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(54) Title: GENETIC ANALYSIS OF PEYERS'S PATCHES AND M CELLS AND METHODS AND COMPOSITIONS TARGETING PEYER'S PATCHES AND M CELL RECEPTORS

(57) Abstract: Methods of increasing of or decreasing the levels of a protein in a PP cell; methods of increasing antigen, vaccine, DNA vaccine delivery to M cells, use of human serum albumin and other transport enhancing proteins to enhance oral drug delivery; use of calreticulin to enhance oral antigen delivery, use of other cell surface proteins, receptors, and transporters to enhance delivery to M cells of antigens or vaccine delivery vehicles, use of other cytoplasmic proteins to regulate intracellular trafficking and delivery to mucosal immune sampling and processing systems.

TITLE OF THE INVENTION

GENETIC ANALYSIS OF PEYER'S PATCHES AND M CELLS AND METHODS AND COMPOSITIONS TARGETING PEYER'S PATCHES AND M CELL RECEPTORS

CROSS REFERENCE TO RELATED APPLICATIONS

This application claims the benefit of U.S. provisional application 60/281,387 filed April 4, 2001, and U.S. provisional application 60/302,591 filed July 2, 2001.

FIELD OF THE INVENTION

This invention relates to the genetic analysis of M cells and methods and compositions targeting M cell receptors.

BACKGROUND OF THE INVENTION

The Peyer's patch of the intestinal lining is a specialized tissue that allows the immune system to identify foreign antigens that require an immune response. It is also a potential pathway for orally delivered drugs to cross the intestinal barrier into the bloodstream. Central to these properties are M cells, which populate the patch's epithelial sheet. In view of the importance of the Peyer's patch and its M cells for the immune response and drug delivery, it is desirable to identify the cell proteins important for these phenomena. It is also desirable to increase the amounts of such important proteins in order to either facilitate the immune response and drug delivery or promote the conversion of non-M cells to M cells.

Similarly, it is important to identify and further decrease the levels of proteins whose absence or down-regulation in expression facilitates the immune response and drug delivery, or promotes the conversion of non-M cells to M cells.

BRIEF SUMMARY OF THE INVENTION

Increasing the levels of a protein or antigen-protein combination

In a first general aspect, the invention is a method of increasing the levels of a protein

in a Peyer's patch cell, said method comprising delivering to said cell a nucleic acid coding for a protein, wherein absent said increase, the levels of said protein or its mRNA is greater than in a non-Peyer's patch cell.

Peyer's patch cells of particular interest are M cells. The levels of a protein or its mRNA in Caco-2 cells co-cultured with Raji B cells are considered herein to be representative of such levels in a human Peyer's patch M cell. Monoculture Caco-2 cells are considered herein to be an appropriate non-Peyer's patch cell for purposes of comparison of such protein or mRNA levels.

The levels of a protein or its mRNA in rat Peyer's patch epithelial cells can be compared to their respective levels in a culture of rat normal gut epithelial cells. Absent evidence to the contrary, results of rat cells are assumed to be predictive of the results in human cells.

The presence of Increased levels of an mRNA, and therefore presumptively its protein, are indicated in the Table 2 and 3 by a **, a *, or an expression Fold Change greater than 1.00. Preferred are those indicated by a ** or an expression Fold Change greater than 2.00. Most highly preferred are those indicated by a **. The presence of decreased levels of an mRNA, and presumptively its protein, are indicated by a minus sign (-) or an expression Fold Change less than 1.00. Preferred targets are those indicated by a minus sign or an expression Fold Change less than 0.50.

In embodiments of particular interest, the protein is a receptor, a transporter, cell surface antigen, or cell adhesion molecule, especially a receptor. In other embodiments of particular interest, the protein is selected from the group consisting of nucleoside diphosphate kinases and member of the 14-3-3 family.

In the methods of greatest interest, the nucleic acid is delivered to a human cell. There are many delivery options, one of which is to deliver it by the oral route with the cell in a human, another to deliver it to a cell outside a human.

In an important variation of the method, a nucleic acid coding for a tumor antigen or foreign peptide is also delivered to the Peyer's patch cell. The purpose of this aspect of the invention is to improve the immune response to a tumor antigen or the foreign peptide. Normally, therefore, the foreign peptide will be that of a virus or infectious microorganism. A tumor antigen is one that is more abundant in a tumor cell than its normal counterpart.

Decreasing the levels of a protein

Another general aspect of the invention is a method of decreasing the levels of a

protein in a Peyer's patch cell, said method comprising delivering to said cell an anti-sense nucleic acid molecule, a ribozyme nucleic acid molecule, an RNA interference (RNAi) nucleic acid molecule, said anti-sense, ribozyme or RNAi nucleic acid being complementary to a sequence of at least 10 nucleotides of the mRNA for said protein, wherein absent said anti-sense nucleic acid molecule, ribozyme or RNAi nucleic acid, the levels of said protein or its mRNA are less than in a non-Peyer's patch cell. More preferably the anti-sense nucleic acid is complementary to a sequence of at least 15 nucleotides of the mRNA of the protein, and most preferably to a sequence of at least 30 nucleotides of the mRNA of the protein. It is preferred that the protein is coded for by a gene with an expression Fold Change denoted by a minus sign (-) or an expression Fold Change less than 0.50.

In a particular embodiment, the latter method comprises delivering to said cell an anti-sense nucleic acid molecules, a ribozyme or RNAi nucleic acid molecules, said anti-sense, ribozyme or RNAi nucleic acid being complementary to a sequence of at least 10 nucleotides of the mRNA for at least 5 different proteins, wherein absent said anti-sense, ribozyme or RNAi nucleic acid molecule, the levels of each of said proteins or its mRNA are less than in a non-Peyer's patch cell.

Alternatively described, the latter invention is a method of deceasing the levels of a protein in a Peyer's patch cell, said method comprising delivering to said cell an anti-sense nucleic acid molecule, ribozyme or RNAi nucleic acid molecules, said anti-sense, ribozyme or RNAi nucleic acid forming a double-stranded molecule with part or all of the mRNA for said protein, wherein absent said anti-sense, ribozyme or RNAi nucleic acid molecule, the levels of said protein or its mRNA are less than in a non-Peyer's patch cell.

Cells of the invention

A human or rat cell to which any of the above methods in this Brief Summary of the Invention section has been applied, or the progeny of said cell, is also an aspect of the present invention.

Delivery enhancement using a targeting ligand which targets a receptor, a transporter or a cell-surface molecule expressed on surface of M cells or Peyer's patch tissue cells

In another general aspect, the invention is a method of targeting an antigen or a drug delivery vehicle containing an antigen, or a drug delivery vehicle containing an antigen and adjuvant, or a drug delivery vehicle containing a drug, or a viral vector, or a bacterio-phage vector such as, but without limitation M13 or Fd, or a bacterial vector or a gene delivery

vector expressing an antigen of interest, or a viral vector, or a bacterio-phage vector such as, but without limitation M13 or Fd, or a bacterial vector or a gene delivery vector expressing a gene product(s) to M cells of Peyer's patch tissue, by targeted delivery to receptors, or to transporters or to other cell surface proteins which are found to be expressed on the cell surface of M cells or other cells found within Peyer's patch tissue, or which are found to be differentially expressed on these cells. Said gene product(s) coded by the viral vector, or a bacterio-phage vector such as, but without limitation M13 or Fd, or a bacterial vector or a gene delivery vector regulate the function of Peyer's patch cells to M cell phenotype or regulate M cell function to increase their immuno-surveillance or antigen presentation to the mucosal immune system.

In one embodiment, a phage display library such as M13 or Fd which express random peptide sequences on the surface of the phage, coded by example gene III or gene VII of M13 or Fd bacteriophage, can be screened by in vivo panning against example Peyer's patch tissue found in vivo in the GIT, in order to discover and identify phage or targeting ligands which specifically target M cells or Peyer's patch tissue in vivo in the GIT; such phage which target M cells and Peyer's patch tissue can subsequently be genetically engineered to encode a gene or genes of interest such as a DNA vaccine gene, a gene coding for an antigen of interest together with gene(s) which modify M cell function and which enhance the immuno-responsiveness of the M cells to the antigen or DNA vaccine product coded by the genetically engineered bacteriophage genome.

Delivery enhancement using transport enhancing proteins

Another invention disclosed herein is a method for enhancing transport of a drug through the gastrointestinal tract, said method comprising orally administering said drug in a composition that comprises a transport-enhancing protein, said transport-enhancing protein selected from the group consisting of human serum albumin (HSA), clusterin, T-cell surface glycoprotein CD5 precursor, HSP84, and Ca^{2+}-dependant phospholipase A_2 (Ca2+pla2), or a homolog that has at least 80% amino acid identity with said transport-enhancing protein over a length of said transport-enhancing protein identical to the homolog. In a preferred embodiment, the homolog has at least 90% amino acid identity with the transport-enhancing protein over a length of the transport-enhancing protein identical to the homolog. In a more preferred embodiment, the transport-enhancing protein is selected from the group consisting of human serum albumin (HSA), clusterin, T-cell surface glycoprotein CD5 precursor, HSP84, and Ca2+pla2.

Method of delivering a vaccine to a target cell

Further invention disclosed herein is a method of delivering a vaccine to a target cell, said method comprising utilizing as the target cell a Peyer's patch cell in which a protein or mRNA is upregulated.

Method of decreasing the levels of a protein

Yet, another invention disclosed herein is a method of decreasing the levels of a protein in a Peyer's patch cell, said method comprising delivering to said cell a DNA molecule coding for an anti-sense nucleic acid molecule, a ribozyme nucleic acid molecule, an RNA interference nucleic acid molecule (RNAi), said anti-sense molecule, ribozyme or RNAi nucleic acid being complementary to a sequence of at least 10 nucleotides of the mRNA for said protein, wherein absent said anti-sense molecule, ribozyme or RNAi nucleic acid , the levels of said protein or its mRNA is less than in a non-Peyer's patch cell.

Method of increasing the extent to which the function of a protein is carried out

Another invention disclosed herein is a method of increasing the extent to which the function of a protein is carried out in a Peyer's patch cell, said method comprising delivering to said cell a nucleic acid coding for said protein, wherein absent said delivery, the level of said protein or its mRNA is greater in said cell than in a non-Peyer's patch cell.

Chimeric protein that comprises two or more segments, each of said segments enhancing a different step in the peptide transport process

Another invention disclosed herein is a chimeric protein that comprises two or more segments, each of said segments enhancing a different step in the peptide transport process, said steps selected from the group consisting of binding to a cell such as an M cell, transporting the peptide into the cell such as an M cell, presenting the chimeric protein to a protein processing pathway within a cell such as an M cell in order to maximise processing in a way to optimize presentation of the processed chimeric peptides to epitopes suitable for immune activation, transporting the peptide through the cell such as an M cell, and transporting the peptide out of the cell such as an M cell to an underlying immune cell such as a B-cell or T-cell.

Delivery enhancement using calreticulin and other proteins

Another method disclosed herein is a method to facilitate intracellular trafficking of an antigen that has been orally delivered by itself or as part of a composition or particle, said method comprising administering calreticulin.

Related to the latter invention is a chimeric protein comprising the amino acid sequences for (1) calreticulin, rab family proteins and and/or a ribosomal protein, and (2) a second polypeptide. Also related is a method of administering a polypeptide, where said polypeptide is part of the chimeric protein and wherein said chimeric protein is orally administered.

DETAILED DESCRIPTION OF THE INVENTION

The present invention and the related research were intended to improve targeted vaccine delivery and targeted gene delivery methods, especially as they relate to Peyer's patch cells. In significant part, this was achieved by identifying proteins whose up-regulation or down-regulation would indicate their possible or probable role in cellular functions important to vaccine and or drug delivery. In some cases, such as receptors, the proteins are important from the point of view of cell specificity during the delivery process. In many cases, the proteins have functions that are important after the vaccine or drug enter the cell.

Closely related to those inventions and research goals, was the concept that in M cells there would be proteins that, as compared to M cell precursors, were up-regulated or down-regulated. The identification of such proteins provides a strategy for altering M cell precursors so as to shift their phenotype toward that of M cells.

As indicated, one aim of the research related to the present invention was to determine if there were detectable differences in protein/gene expression between: (1) Peyer's patch (PP) and non-Peyer's patch (NPP) rat gastrointestinal tract (GIT) tissue and (2) M cell enriched follicle-associated epithelium of Peyer's patch (PP FAE) tissue. This was done with a view to finding novel or highly expressed ligand targeting sites on the Peyer's patch or M cells as well as other protein relevant to the delivery of drugs across the GIT.

This invention is based in part on the discovery of over-expression of a range of genes in Peyer's patch (PP) tissue from rat small intestine in comparison to normal non-Peyer's patch (NPP) small intestine tissue.

This invention is also based on the discovery of over-expressed genes in co-cultures of Caco-2 cells. The idea was to use genetic mapping of the M cell co-culture, e.g. Caco-2

cells co-cultured with Raji cells versus a monolayer of Caco-2 cells, to ascertain the differences in epithelial gene expression between M cells and enterocytes. It became immediately apparent that some of these gene products are going to be unique apical membrane proteins (e.g. receptors, transporters, adhesion proteins) in M cells. By examining the differences between M cells and enterocytes in vitro and in vivo, one could identify key targets that can be used to generate M cell specific ligands. These ligands can then be used for targeting oral vaccines in particles.

The identification of over-expressed ribosomal proteins or homologues/related proteins thereof indicates a generally higher protein turnover or protein synthesis capacity in PPs or a possible role for such ribosomal proteins (or homologues thereof) in other cellular functions such as protein chaperoning, endocytosis, trafficking of proteins/antigens/particulates/viruses uptaken from the lumen of the gastrointestinal tract (GIT) and/or from the M cells to underlying immune cells, antigen presenting cells, dendritic cells, B cells, other cell types.

The identification of a series of transcription factors (TFs) that are over-expressed in PP tissue versus the control enterocyte GIT tissue is considered herein to indicate a role for such TFs in the development of M cell phenotype, in conferring M cell phenotype and/or in programming M cells to prime other downstream cellular events leading to a better or more efficacious immune outcome following antigen presentation. The co-delivery of genes coding for such TFs with either antigens themselves and /or with gene(s) coding for antigen(s) of question to M cells and/or PP tissue following oral administration provides the basis for a more efficacious and pronounced immune outcome when the TF coding genes are key or vital for driving M cells / PP tissue to an effective immune outcome.

The general over-expression of a number of proteins species in PPs versus NPPs, both membrane and cytosolic-associated was also determined by a novel technique of enrichment and M cell selection following enrichment of the follicle-associated epithelium (FAE) of Peyer's patch (PP FAE) by ethylene-diamine tetra-acetic acid (EDTA) extraction and recovery of M cells / PP FAE. Such novel or differentially expressed proteins have significant implications for the use of this protein expression information and methods of selection / enrichment of M cells / PP tissue for the targeting of drug/vaccine uptake to Peyer's patches. Among proteins found to be over expressed in rat PP tissue following this enrichment technique was the human serum albumin homolog which is considered here to have implications for drug / cargo transport from the GIT either into or across intestinal tissue including PP tissue and systemic delivery of same to the blood.

Incorporation by reference

All references cited herein are incorporated herein by reference in their entireties.

All GenBank records specified by their accession numbers are incorporated herein by their entireties.

The GenBank amino acid sequences and nucleotide sequences specified by their GenBank ID number are incorporated by reference herein. All GenBank records corresponding to those ID numbers are incorporated herein in their entirety. Absent a date specifying the date of the record, the date of the record is the filing date of this application.

Many of GenBank sequences specified by their GenBank ID numbers are reproduced herein in the section "Amino acid sequences and nucleotide sequences corresponding to selected GenBank ID numbers." The CDS line refers to the exon(s).

Any GenBank ID numbers specified herein, absent a decimal point and an integer following that decimal point, is for GenBank version 1 of that sequence. Any GenBank ID number that has a decimal point and an integer following it is the GenBank version number.

The invention will be illustrated in more details with reference to the following Examples, but it should be understood that the present invention is not deemed to be limited thereto.

EXAMPLES

Example 1

Preparation of cytosolic (S100) and membrane (P100) proteins from rat PP and NPP tissues

Protein samples were prepared from PP and NPP tissue extracted from freshly sacrificed rats. These protein samples underwent electrophoresis on denatured SDS-PAGE gels and were stained using two different standard proteins Commassie Blue stains. Subsequently, fresh PP and NPP tissue samples were fractionated into cytosolic (S100) and membrane (P100) proteins and these samples were also electrophoresed on SDS-PAGE in order to compare S100 and P100 fractions in both PP and NPP tissues.

Example 2

Preparation of GIT tissue or co-culture cell membrane (P100) and cytosolic (S100) fractions

The fractions were prepared using the following procedure:

1. Scrape the co-culture cells into PBS and pool cells into a universal.
2. Centrifuge the cells for 5 minutes at 1,500 rpm.
3. Remove the supernatant.
4. Re-suspend the cell pellet in 3 volumes of ice-cold HED buffer, and allow it to swell for 5 minutes on ice.
5. Homogenize the cells for 30 seconds.
6. Centrifuge the homogenate in hard walled tubes at 40,000rpm for 45minutes at 4°C in a Beckmann Ultra Centrifuge (rotor Ti90).
7. Remove the supernatant (S100) and re-suspend the pellet (P100) in 3 volumes of HEDG buffer, before centrifugation again at 1000rpm for 2min. Remove the supernatant and store on ice. Repeat the procedure and add the second supernatant to the first.
8. Determine the protein concentration (using the Bio-Rad protein assay).
9. All fractions were stored at –80°C.

The following reagents were used in the above methods:

HED buffer (20mM HEPES pH 7.67), 1mM EGTA, 0.5mM dithiothreitol, 1mM phenylmethylsulphonyl fluoride (PMSF):

HEPES (pH to 7.67)	0.5206g
EGTA	38.04mg
Dithiothreitol	7.71 mg

Distilled water	to 100ml

10µl PMSF stock solution was added to 1ml of buffer prior to use.

HEDG buffer (the same as HED buffer plus 100mM NaCl, 10% glycerol)

NaCl	0.584g
Glycerol	11.4ml
HEPES (pH to 7.67)	0.5206g
EGTA	38.04mg
Dithiothreitol	7.71 mg
Distilled water	to 100ml

10µl PMSF stock solution was added to 1ml of buffer prior to use.

PMSF(100mM) stock solution

PMSF	17.42mg
Isopropanol	

Example 3

Isolation of epithelial sheaths from rat Peyer's patch and non-Peyer's patch tissue

The M cell is a very elusive cell type, at least in terms of isolating a purified population. Previous attempts have found that when M cells are separated and purified and put into culture they very quickly lose their characteristic morhphology and probably gene/protein expression profile. In many cases this is due to the length of time taken to isolate and purify the cells from the very homogenous mix of cells in a Peyer's patch. We desired a quick and routine method to enrich for M cells is Peyer's patch samples. M cells are only contained in the epithelium of Peyer's patches, the so-called follicle associated epithelium (FAE), while underneath the epithelial layer lays all the B and T lymphocytes, dendritic cells etc. So by isolating the epithelium away from the rest of the Peyer's patch dome, we are greatly enriching it for the M cell population. Previously, treatment of mouse intestinal tissue with EDTA was shown to cause separation of the epithelium as a sheet from the rest of the tissue, allowing for it's specific isolation (Bjerknes M and Cheng H (1981). Methods for the isolation of intact epithelium from the mouse intestine. *Anat. Rec.*, (199):565). This method was adapted for the isolation of FAE from rat Peyer's patch. Control epithelium from normal gut tissue (no Peyer's patches) was used as a control.

Epithelial sheaths were prepared using EDTA method comprising the following steps:

1. Sacrifice the rats (Wistar) by cervical dislocation.
2. Remove the entire length of the GIT tract from (but not including) the stomach to the caecum and place in a dish of PBS (at room temperature).
3. Excise the Peyer's patches, taking care to remove as much normal non-PP GI tissue as is visible. Rinse briefly in PBS.
4. Also take samples of normal non-Peyer's (NPP) tissue close to the patches, rinse in PBS and treat as for the PPs (steps 5-9, 11-12).
5. Pool the PP's from the entire GI section in Hank's Buffered Saline Solution (HBSS, Gibco Life Sciences) with 0.011M glucose and 25mM Hepes.
6. When pooling is complete, place PP sections into 15-20ml of HBSS (with 0.011M glucose and 25mM Hepes) along with 40mM of EDTA into a small conical flask.
7. Add a stirrer bar to the flask, place on a stirring plate and spin the PP's for 15 min at RT.
8. After 15 minutes pipette the PP solution vigorously with a wide-bore 3ml plastic pasteur pipette.
9. Strain the supernatant through a 100micron nylon cell strainer (from FALCON™, 352360).
10. Move the filter to another 50ml tube and wash out the residue material on the filter with HBSS (with 0.011M glucose and 25mM Hepes, no EDTA). This residue contains the majority of the PP dome epithelial sheaths.
11. Centrifuge the PP residue material at 3000 rpm for 5min. Also centrifuge the NPP tissue supernatant at 3000 rpm for 5min.
12. Snap freeze the cell pellets and store at –70°C.

Example 4

Identification of over-expressed proteins in enriched M cells / PP FAE cells

Epithelial cell layers of Wistar rat PP (representing enriched M cells / PP FAE cells) and normal villi were extracted using EDTA as described in Example 3 above. Epithelial layers from numerous Patches and rats were pooled and the protein isolated into either cytosolic and membrane fractions following centrifugal separation. 2D gel electrophoresis (between isoelectric points pH 3.5 to 10) was performed on 50 µg of each fraction, wherein the gels were silver stained. The gels were overlaid, and numerous differentially expressed

proteins between the membrane fractions of PP and normal villi epithelia were observed. Further, protein samples underwent a second 2D gel electrophoresis, this time the gel was stained with a "special" silver stain, that did not inhibit the mass spectrometry analysis of individual spots. The differentially expressed proteins were identified and highlighted by gel overlay.

Thirty-seven protein spots were identified that were increased in PP over villi epithelial membrane fractions. Of these, 16 spots (the most highly over-expressed) were chosen for mass spectrometry analysis. The spots were digested with endoproteinase Lys-C/trypsin (8:1 ratio) and analyzed on a MALDI-MS. The spots, however, gave very poor spectra and only 4 of the 16 were identifiable. These were:

serum albumin;

calreticulin;

14-3-3 zeta (tentative ID; mouse); and

nucleoside diphosphate kinase B.

One protein showed homology to human serum albumin (HSA). Work by A. Fasano at Maryland had suggested that Zonulin, the human homologue of ZOT, showed sequence homology to human serum albumin (85% homology across the limited sequence available from the Fasano's work). Given our finding that a protein differentially expressed in rat PP tissue shows homology to HSA, we propose that HSA (or a homologue or splice variant thereof) is involved in drug transport in the GIT, in particular Peyer's patch tissue of the GIT.

Calreticulin is a 46-kDa Ca (2+)-binding chaperone of the endoplasmic reticulum membranes. This protein binds Ca (2+) with high capacity, affects intracellular Ca (2+) homeostasis, and functions as a lectin-like chaperone. Given the over-abundance of expression of this protein in epithelial layers selected from PP tissue and the role of this protein as a lectin-like chaperone, we propose that this protein is a valuable protein target to aid or facilitate the intracellular trafficking of antigens or antigens in particles following targeted delivery to M cells or PP tissue. Proteins comprising chimerics of calreticulin plus a polypeptide with an antigen of choice would therefore prove valuable in that regard.

Members of the 14-3-3 protein family have been identified as regulatory elements in intracellular signaling pathways and cell cycle control. There had been reports that 14-3-3 protein can be used as a marker for Creutzfeldt-Jacob Disease (CJD) in cerebrospinal fluid (CSF). It is proposed that this protein or the gene coding for it is valuable in the control of the M cell phenotype, and as a result it would be advantageous to co-deliver that protein or gene with a protein, antigen, or DNA vaccine.

Nucleoside diphosphate kinases (NDP kinases) form a family of oligomeric enzymes present in all organisms. Eukaryotic NDP kinases are hexamers composed of identical subunits (approximately 17 kDa). A distinctive property of human NDPK-B is its ability to stimulate gene transcription. This property is independent of its catalytic activity and is possibly related to the role of this protein in cellular events including differentiation and tumor metastasis. Given our discovery of the increased expression of nucleoside diphosphate kinase B in M cell enriched PP FAE cells, we propose the importance of this protein in determining or controlling M cell phenotype, in M cell development, and optimal activation or priming of the mucosal immune system.

Example 5

Gene expression analysis of rat PP and NPP tissue samples

In addition to the proteomic studies highlighted above, PP and NPP tissue samples were sent for gene expression analysis to CLONTECH Laboratories Inc. (a division of Becton Dickinson (BD) Biosciences) who then extracted RNA from the tissues to probe on ATLAS™1.2 rat arrays. The data containing differential expression levels of 1,200 genes many of which are presented in Table 1 below. The data show over-expression of many proteins. In Table 1, over-expressed genes are shown in bold and italicized.

In Table 1, "N/C" means not calculated due to manually-determined inconsistencies in one or both spots, and "?" means low confidence level (small difference).

Also, over-expressed genes from Table 1 that had a fold change above 0, as well as over-expressed genes are shown in Table 2 below with corresponding GenBank accession numbers for rat and human origin.

Based on the results (ratio PP/ Normal epithelial tissue) in Table 1, the following proteins are of the particular interest: clusterin, T-cell surface glycoprotein CD5 precursor, HSP84, Ca2+-dependant phospholipase A2 precursor, ribosomal proteins S12, S11, L12, L11, S29, S19, L21, L19, L13, L44, and L36A.

In addition a series of genes coding for different TFs was noted including the following:

Jun-B; c-jun related TF,

Jun-D; c-jun related TF,

STAT 3 - signal transducer and activator of transcription 3,

NF-kappaβ Tf p105 subunit,

CREB active TF,
New england deaconess TF,
C-jun proto-oncogene; TF AP-1; RJG-9,
S-myc proto-oncogene; myc related,
Nm23-M2; nucleoside diphosphate kinase B; metastasis reducing protein,
NDK-B; nucleoside diphosphate kinase B ; metastasis reducing protein,
Lim-2; embryonic motor neuron topographic organizer; homeobox protein LIM-2, and
C-est-I proto-oncogene; p54.

TF coding genes such as these are considered here to be important in the development of M cell phenotype and in priming the immune system. Their co-delivery or co-targeting with DNA vaccine genes and/or with vaccines is expected to enhance activation of mucosal immunity to the co-delivered DNA vaccine and/or antigen by virtue of their priming of the cells to give a better mucosal immunity outcome.

TABLE 1

GENE EXPRESSION DATA FROM ATLAS 1.2 RAT ARRAY ANALYSIS

#	coordinate	Spot Intensity PP1	Spot Intensity NE1	RATIO	Difference	GENE
1	A03c	38	6	0.16	-32	***T-cell surface glycoprotein CD5 precursor; lymphocyte glycoprotein LY1***
2	A03g	31	57	1.84	26	CD4 homologue, W3/25 antigen
3	A04f	20	72	3.60	52	signal transducer CD24 precursor; heat stable antigen (HSA); nectadrin
4	A04i	17	40	2.35	23	CD2, membrane glycoprotein, T-cell marker
5	A04j	8	34	4.25	26	scavenger receptor class B type I
6	A04m	16	31	1.94	15	SR13 myelin protein; peripheral myelin protein 22 (PMP-22); CD25 protein
7	A05a	4	17	4.25	13	glutamyl aminopeptidase A
8	A05i	52	29	0.56	-23	***I-kB (I-kappa B) alpha chain; RL/IF-1 gene product***
9	A05m	6	18	3.00	12	interferon regulatory factor 1 (IRF1)
10	A06a	7	21	3.00	14	LIM domain protein CLP36, homologous to rat RIL
11	A06c	152	78	0.51	-74	Gax, growth-arrest-specific protein
12	A07c	42	24	0.57	-18	***G1/S-specific cyclin D3 (CCND3)***
13	A07l	17	3	0.18	-14	***M-phase inducer phosphatase 2 (MPI2); cell division control protein 25 B (CDC25B)***
14	A07n	37	20	0.54	-17	***p55cdc; cell division control protein 20***
15	A08e	56	24	0.43	-32	***prothymosin-alpha (PTMA)***
16	A08n	32	105	3.28	73	antigen peptide transporter 1
17	A09g	13	36	2.77	23	proteasome delta subunit precursor; macropain delta; multicatalytic endopeptidase complex delta;
18	A09i	15	27	1.80	12	proteasome component C13 precursor; macropain subunit C13; multicatalytic endopeptidase
19	A09j	341	893	2.62	552	apolipoprotein A-I precursor (APO-AI)
20	A09k	72	723	10.04	651	apolipoprotein A-IV precursor (APO-AIV)
21	A11l	1	13	13.00	12	ErbB3 EGF receptor-related proto-oncogene; HER3
22	A12c	21	48	2.29	27	A-raf proto-oncogene
23	A12i	19	45	2.37	26	rac-alpha serine/threonine kinase (RAC-PK-alpha); protein kinase B (PKB); AKT1
24	A13k	208	60	0.29	-148	***HSP84; HSP90-beta; heat shock 90kD protein***
25	A14c	7	38	5.43	31	glutathione S-transferase Ya subunit (GST YA); ligandin subunit 1 alpha
26	A14d	65	162	2.49	97	microsomal glutathione S-transferase (GST12; MGST1)
27	A14e	94	160	1.70	66	glutathione S-transferase Yb subunit; GST subunit 4 mu (GSTM2)
28	A14g	129	265	2.05	136	glutathione S-transferase P subunit; GST subunit 7 pi (GST7-7)
29	A14n	7	19	2.71	12	NADPH-cytochrome P450 reductase (CPR); POR
30	B01h	121	207	1.71	86	copper-zinc-containing superoxide dismutase 1 (Cu-Zn SOD1)
31	B02f	4	25	6.25	21	fructose (glucose) transporter
32	B05k	13	36	2.77	23	sodium channel SCNB2, beta 2 subunit, brain
33	B06d	28	12	0.43	-16	***potassium channel, inward rectifier 11***
34	B07k	2	18	9.00	16	proton-coupled dipeptide cotransporter
35	B08b	59	181	3.07	122	fibroblast ADP/ATP carrier protein; ADP/ATP translocase 2; adenine nucleotide translocator 2
36	B09i	7	43	6.14	36	sodium-glucose cotransporter 1
37	B09l	40	115	2.88	75	Na+/K+ ATPase alpha 1 subunit
38	B09n	43	78	1.81	35	vacuolar ATP synthase 16-kDa proteolipid subunit; ATP6C; MVP; ATPL
39	B10b	10	78	7.80	68	sodium/potassium-transporting ATPase beta 1 subunit (ATP1B1)
40	B12e	10	68	6.80	58	urate transporter/channel
41	B12f	143	297	2.08	154	ATP synthase lipid-binding protein P1 precursor; ATPase protein 9; ATP5G1
42	B12g	21	112	5.33	91	ATP synthase, subunit c, P2 gene
43	B12m	18	38	2.11	20	annexin IV(ANX4); lipocortin IV;36-kDa zymogen granule membrane-associated protein (ZAP36)
44	B13f	37	127	3.43	90	lipocortin 2
45	B14d	59	326	5.53	267	fatty acid-binding protein (liver; L-FABP); Z-protein; squalene- & sterol-carrier protein (SCP); P14
46	B14f	49	157	3.20	108	fatty acid-binding protein (intestinal; I-FABP; FABPI)

#	coordinate	Spot Intensity PP1	NE1	RATIO	Difference	GENE
47	C02f	19	78	4.11	59	fructose-bisphosphate aldolase B (ALDOB); liver-type aldolase
48	C02g	37	76	2.05	39	fructose-bisphosphate aldolase A (ALDOA); muscle-type aldolase
49	C02j	15	30	2.00	15	testis fructose-6-phosphate 2-kinase/fructose 2,6-biphosphate (testis 6PF-2-K/fru-2,6-P2ase); 6-
50	C02n	604	1123	1.86	519	cytochrome c oxidase subunit Vb & VIa precursor (COX5B)
51	C03a	9	20	2.22	11	cytochrome B5 (CYB5)
52	C03e	65	138	2.12	73	mitochondrial hydroxymethylglutaryl-CoA synthase precursor (HMG-CoA synthase); 3-hydroxy-3-
53	C03f	177	760	4.29	583	cytochrome oxidase, subunit I, Sertoli cells
54	C03g	27	47	1.74	20	ATPase, subunit F, vacuolar (vatf)
55	C03i	641	1087	1.70	446	cytochrome c oxidase, subunit IV, mitochondrial
56	C03j	46	147	3.20	101	cytochrome c oxidase, subunit Va, mitochondrial
57	C03l	317	180	0.57	-137	***cytochrome c oxidase, subunit VIIIh***
58	C04b	189	351	1.86	162	mitochondrial ATP synthase beta subunit precursor (ATP5B)
59	C04g	23	127	5.52	104	creatine kinase, ubiquitous, mitochondrial
60	C06c	6	52	8.67	46	fatty acid amide hydrolase
61	C06j	73	175	2.40	102	cytochrome P450 17 (CYP17); P450C17; CYPXVII; steroid 17-alpha-hydroxylase/17,20 lyase
62	C07i	9	51	5.67	42	cytochrome P-450 4F1, hepatic tumour
63	C07j	19	39	2.05	20	cytochrome P-450 4F4
64	C08a	17	33	1.94	16	cytochrome P-450 4F5
65	C08l	8	24	3.00	16	adenylate kinase 3
66	C08m	32	65	2.03	33	cAMP-dependent protein kinase type I-alpha regulatory chain
67	C09e	7	30	4.29	23	glutathione synthetase (GSH synthetase; GSH-S; GSS); glutathione synthase
68	C10e	25	10	0.40	-15	***carbonic anhydrase 4***
69	C10j	19	9	0.47	-10	***alkaline phosphatase***
70	C10k	21	5	0.24	-16	***dopamine beta-hydroxylase***
71	C10l	29	11	0.38	-18	***acetylcholinesterase, T subunit, glycolipid-anchored***
72	C10m	228	445	1.95	217	NADP+ alcohol dehydrogenase; aldehyde reductase (ALR); 3-dG-reducing enzyme
73	C11b	19	33	1.74	14	calcium binding protein 2 (CABP2); endoplasmic reticulum stress protein (ERP72); protein disulfide
74	C11d	97	55	0.57	-42	***60S ribosomal protein L44; L36A***
75	C11e	1728	527	0.30	-1201	***40S ribosomal protein S12***
76	C11g	400	179	0.45	-221	***ribosomal protein L11***
77	C11h	670	355	0.53	-315	***ribosomal protein L13***
78	C11j	967	424	0.44	-543	***ribosomal protein L12***
79	C11k	812	413	0.51	-399	***S19; 40S ribosomal protein S19***
80	C11l	554	286	0.52	-268	***60S ribosomal protein L21***
81	C11m	1405	737	0.52	-668	***60S ribosomal protein L19 (RPL19)***
82	C11n	315	109	0.35	-206	***40S ribosomal protein S11***
83	C12b	158	48	0.30	-110	***Fte-1; putative v-fos transformation effector protein; yeast mitochondrial protein import homolog; 40S***
84	C12d	1451	787	0.54	-664	***elongation factor 2 (EF2)***
85	C12l	346	10	0.03	-336	***clusterin (CLU); testosterone-repressed prostate message 2 (TRPM2); apolipoprotein J; sulfated***
86	C12m	14	0	Undefined	-14	***activator of apoptosis harakiri (HRK); neuronal death protein 5 (DP5); BID3***
87	C13c	19	5	0.26	-14	***SURVIVAL OF MOTOR NEURON(RSMN)***
88	D08i	6	17	2.83	11	retinoid X receptor alpha (RXR alpha; RXRA); NR2B1
89	D12c	6	18	3.00	12	INOSITOL TRIPHOSPHATE RECEPTOR SUBTYPE 3
90	E01m	10	50	5.00	40	neurotrophin 3 precursor (NTF3); neurotrophic factor; HDNF; nerve growth factor 2 (NGF2)
91	E02c	19	8	0.42	-11	***transforming growth factor, beta 1***
92	E03k	40	185	4.63	145	C-type natriuretic peptide precursor (CNP; NPPC)
93	E04b	17	7	0.41	-10	***thyroid stimulating hormone, beta***
94	E07c	33	15	0.45	-18	***c-src-kinase (CSK) & negative regulator; tyrosine-protein kinase***

#	coordinate	Spot Intensity PP1	NE1	RATIO	Difference	GENE
95	E08a	105	249	2.37	144	extracellular signal-regulated kinase 1 (ERK1); mitogen-activated protein kinase 1 (MAP kinase 1;
96	E08l	8	22	2.75	14	protein kinase C delta type (PKC-delta)
97	E09j	36	68	1.89	32	insulin receptor-related receptor-alpha (sIRR-1)
98	E10f	3	17	5.67	14	CamK II; calcium/calmodulin-dependent protein kinase brain type II beta
99	E10g	3	13	4.33	10	CamK I; calcium/calmodulin-dependent protein kinase type I + CaM-like protein kinase
100	E10j	18	42	2.33	24	Casein kinase I delta; CKId; 49-kDa isoform
101	E11e	15	29	1.93	14	cyclin-dependent kinase 4 (CDK4); cell division protein kinase 4; PSK-J3
102	E12g	23	45	1.96	22	protein phosphatase 2C isoform; Mg2+ dependent protein phosphatase beta isoform
103	E13i	40	19	0.48	-21	***guanine nucleotide-binding protein G(I) alpha 2 subunit (GNAI2); adenylate cyclase-***
104	E14i	268	661	2.47	393	rab12, ras related GTPase
105	F01e	10	29	2.90	19	RalGDSB; GTP/GDP dissociation stimulator for a ras-related GTPase
106	F02a	189	97	0.51	-92	***calcium-dependent phospholipase A2 precursor (PLA2); phosphatidylcholine 2-***
107	F02h	15	79	5.27	64	phospholipase C beta 3 (PLC-beta 3)
108	F04e	33	57	1.73	24	14-3-3 protein zeta/delta; PKC inhibitor protein-1; KCIP-1; mitochondrial import stimulation factor
109	F04k	15	29	1.93	14	14-3-3 protein epsilon; PKC inhibitor protein-1; KCIP-1; mitochondrial import stimulation factor L
110	F05e	8	21	2.63	13	presenilin 1 (PSNL1; PSEN1; PS1); S182 protein
111	F05i	6	17	2.83	11	PDGF-associated protein
112	F06a	59	143	2.42	84	ADP-ribosylation factor 5 (ARF5)
113	F06j	12	22	1.83	10	dipeptidase (DPEP1)
114	F07m	7	29	4.14	22	granzyme M precursor (GZMM); MET-ASE; natural killer cell granular protease; RNK-MET-1
115	F08e	11	100	9.09	89	angiotensin converting enzyme (ACE; somatic; dipeptidyl carboxypeptidase I; kininase II
116	F08h	18	48	2.67	30	amonipeptidase B
117	F08j	39	92	2.36	53	kidney aminopeptidase M (APM)
118	F08k	19	81	4.26	62	metalloendopeptidase meprin beta subunit
119	F08l	5	15	3.00	10	endothelin converting enzyme
120	F09a	3	16	5.33	13	gelatinase A
121	F09g	13	27	2.08	14	cathepsin L
122	F09l	14	28	2.00	14	proteasome component C3
123	F12a	6	16	2.67	10	leukocyte common antigen-related tyrosine phosphatase (LAR)
124	G31	12	39	3.25	27	ornithine decarboxylase (ODC)
125	G43	287	1132	3.94	845	cytoplasmic beta-actin (ACTB)
126	G47	7327	3614	0.49	-3713	***40S ribosomal protein S29 (RPS29)***

Table 2
RAT GENES (PP VS. NPP)

GENE	Fold change	GenBank ID Human	GenBank ID Rat
activator of apoptosis harakiri (HRK); neuronal death protein 5 (DP5); BID3	**	U76376.1	D83697
RET ligand 1 (RET1)	**	-	U97142
P2X purinoceptor 1; ATP receptor P2X1; purinergic receptor; RP-2 protein	**	P51575	U14414
leukocyte common antigen precursor (LCA); CD45 antigen; T200; PTPRC	**	Y00638	M10072
amphiphysin II (AMPH2)	**	AF001383.1	Y13380
Jak3 tyrosine-protein kinase; Janus kinase 3	**	XM_038595.3	D28508
DCC; netrin receptor; immunoglobulin gene superfamily member; former tumor suppressor protein candidate	**	M32292.1	AH002168.1
c-fgr proto-oncogene	**	AAA52762.1	X57018.1
small inducible cytokine A3 precursor (SCYA3); macrophage inflammatory protein 1 alpha precursor (MIP1-alpha; MIP1A)	**	P10147	AF119381.1
protein kinase C beta-I type (PKC-beta I) + protein kinase C beta-II type (PKC-beta II)	**	X06318	P04410
E-selectin precursor; endothelial leukocyte adhesion molecule 1 (ELAM-1); leukocyte-endothelial cell adhesion molecule 2 (LECAM2); CD62E	**	P16581	L25527
T-cell receptor CD3 zeta subunit	**	J04132.1	L08447.1
Protein kinase C-binding protein beta15; RING-domain containing	**	-	U48248
G1/S-specific cyclin C (CCNC)	**	AAC50825.1	D14013
maspin; protease inhibitor 5 (PI5); tumor suppressor	**	U04313.1	U58857
peptide/histidine transporter	**	-	AB000280
acetyl-CoA carboxylase (ACC); biotin carboxylase	**	X68968.1	AH002123.1
fibroblast growth factor receptor subtype 4	**	L03840.1	M91599
LCR-1; putative chemokine and HIV coreceptor homolog; G protein-coupled receptor	**	-	U54791
tumor necrosis factor alpha precursor (TNF-alpha; TNFA); cachectin	**	AF043342.1	X66539
CC chemokine MIP3 alpha exodus	**	-	U90447.1
luteinizing hormone, alpha	**	NM_000735.2	V01252
Ctk; non-receptor protein tyrosine kinase (batk)	**	P42679	L34542.1
RhoGAP; p122	**	-	S54293
Adenylyl cyclase type V	**	M83533.1	M96159
cathepsin S precursor (CTSS)	**	P25774	L03201.1
O-6-methylguanine-DNA methyltransferase (MGMT); methylated-DNA-protein-cysteine methyltransferase	**	M31767.1	NM_012861.1
clusterin (CLU); testosterone-repressed prostate message 2 (TRPM2); apolipoprotein J; sulfated glycoprotein 2 (SGP2); dimeric acid glycoprotein (DAG)	34.60	X14723	U02391.1
T-cell surface glycoprotein CD5 precursor; lymphocyte glycoprotein LY-1 (LYT1)	6.33	X04391.1	D10728
M-phase inducer phosphatase 2 (MPI2); cell division control protein 25 B (CDC25B)	5.67	S78187.1	D16237
dopamine beta-hydroxylase	4.20	Y00096.1	L12407

GENE	Fold change	GenBank ID Human	GenBank ID Rat
SURVIVAL OF MOTOR NEURON(RSMN)	3.80	AAC50473.1	U75369
HSP84; HSP90-beta; heat shock 90kD protein	3.47	XM_055551.3	S45392
Fte-1; putative v-fos transformation effector protein; yeast mitochondrial protein import homolog; 40S ribosomal protein S3A ; RPS3A	3.29	M84711.1	M84716.1
40S ribosomal protein S12	3.28	X53505	M18547
40S ribosomal protein S11	2.89	X06617	K03250
acetylcholinesterase, T subunit, glycolipid-anchored	2.64	M55040.1	X71089.1
carbonic anhydrase 4	2.50	NM_000717.2	I52551
thyroid stimulating hormone, beta	2.43	S70587.1	M13897.1
transforming growth factor, beta 1	2.38	M34057	NM_021578.1
prothymosin-alpha (PTMA)	2.33	AF257099.1	M20035
potassium channel, inward rectifier 11	2.33	-	D42145
ribosomal protein L12	2.28	L06505.1	X53504.1
ribosomal protein L11	2.23	X79234.1	X62146.1
c-src-kinase (CSK) & negative regulator; tyrosine-protein kinase	2.20	X59932.1	X58631
alkaline phosphatase	2.11	AAA98616.1	S18408
guanine nucleotide-binding protein G(I) alpha 2 subunit (GNAI2); adenylate cyclase-inhibiting G alpha protein	2.11	XM_041507.1	NM_031035.1
40S ribosomal protein S29 (RPS29)	2.03	NM_001032.2	X59051
S19; 40S ribosomal protein S19	1.97	P39019	P17074
Gax, growth-arrest-specific protein	1.95	-	Z17223.1
calcium-dependent phospholipase A2 precursor (PLA2); phosphatidylcholine 2-acylhydrolase (PLA2-10; PLA2G5)	1.95	M22430.1	U38376.1
60S ribosomal protein L21	1.94	P46778	M27905
60S ribosomal protein L19 (RPL19)	1.91	X63527	J02650
ribosomal protein L13	1.89	P26373	X78327.1
p55cdc; cell division control protein 20	1.85	AF099644.1	AF052695.1
elongation factor 2 (EF2)	1.84	X51466	Y07504.1
I-kB (I-kappa B) alpha chain; RL/IF-1 gene product	1.79	X63594.1	AF388201.1
60S ribosomal protein L44; L36A	1.76	M15661	P10661
cytochrome c oxidase, subunit VIIIh	1.76	J04823.1	NM_012786.1
G1/S-specific cyclin D3 (CCND3)	1.75	NM_001760.2	NM_012766.1
cytochrome c oxidase, subunit IV, mitochondrial	0.59	AF017115.1	X14209
glutathione S-transferase Yb subunit; GST subunit 4 mu (GSTM2)	0.59	-	X04229.1
copper-zinc-containing superoxide dismutase 1 (Cu-Zn SOD1)	0.58	-	NM_017050.1
14-3-3 protein zeta/delta; PKC inhibitor protein-1; KCIP-1; mitochondrial import stimulation factor S1 subunit	0.58	U28964.1	L07913.1
calcium binding protein 2 (CABP2); endoplasmic reticulum stress protein (ERP72); protein disulfide isomerase-related protein precursor	0.58	XM_012077.4	M86870
ATPase, subunit F, vacuolar (vatf)	0.57	AF047436.1	U43175.1
proteasome component C13 precursor; macropain subunit C13; multicatalytic endopeptidase complex subunit C13; PSMB8	0.56	P28062	NM_080767.1
vacuolar ATP synthase 16-kDa proteolipid subunit; ATP6C; MVP; ATPL	0.55	NM_001695.1	M62762.1

GENE	Fold change	GenBank ID Human	GenBank ID Rat
dipeptidase (DPEP1)	0.55	NM_004413.1	M94056
CD4 homologue, W3/25 antigen	0.54	BC025782.	M15768.1
mitochondrial ATP synthase beta subunit precursor (ATP5B)	0.54	NM_001686.1	M19044.1
cytochrome c oxidase subunit Vb & VIa precursor (COX5B)	0.54	M59250.1	X14208.1
insulin receptor-related receptor-alpha (sIRR-1)	0.53	-	M90660.1
cyclin-dependent kinase 4 (CDK4); cell division protein kinase 4; PSK-J3	0.52	P11802	P35426
14-3-3 protein epsilon; PKC inhibitor protein-1; KCIP-1; mitochondrial import stimulation factor L subunit	0.52	XM_088041.1	D30739.1
SR13 myelin protein; peripheral myelin protein 22 (PMP-22); CD25 protein	0.52	-	M69139.1
cytochrome P-450 4F5	0.52	-	AF288818.1
NADP+ alcohol dehydrogenase; aldehyde reductase (ALR); 3-dG-reducing enzyme	0.51	J04794.1	D10854.1
protein phosphatase 2C isoform; Mg2+ dependent protein phosphatase beta isoform	0.51	-	S90449.1
testis fructose-6-phosphate 2-kinase/fructose 2,6-biphosphate (testis 6PF-2-K/fru-2,6-P2ase); 6-phosphofructo- 2-kinase; fructose-2,6-bisphosphatase	0.50	NM_002625.1	X15579.1
proteasome component C3	0.50	D00760	J02897.1
cAMP-dependent protein kinase type I-alpha regulatory chain	0.49	P10644	P09456
cytochrome P-450 4F4	0.49	-	U39206.1
fructose-bisphosphate aldolase A (ALDOA); muscle-type aldolase	0.49	XM_043948.2	NM_012495.1
glutathione S-transferase P subunit; GST subunit 7 pi (GST7-7)	0.49	-	X02904.1
ATP synthase lipid-binding protein P1 precursor; ATPase protein 9; ATP5G1	0.48	NM_005175.1	NM_017311.1
cathepsin L	0.48	M20496.1	Y00697.1
annexin IV(ANX4); lipocortin IV;36-kDa zymogen granule membrane-associated protein (ZAP36)	0.47	XM_031596.3	NM_024155.1
mitochondrial hydroxymethylglutaryl-CoA synthase precursor (HMG-CoA synthase); 3-hydroxy-3-methylglutaryl-CoA synthase; HMGCS2	0.47	P54868	P22791
cytochrome B5 (CYB5)	0.45	M22865.1	D13205.1
A-raf proto-oncogene	0.44	P10398	X06942
Casein kinase I delta; CKId; 49-kDa isoform	0.43	P48730	Q06486
CD2, membrane glycoprotein, T-cell marker	0.43	M14362.1	X05111.1
kidney aminopeptidase M (APM)	0.42	XM_087746.1	M26710
rac-alpha serine/threonine kinase (RAC-PK-alpha); protein kinase B (PKB); AKT1	0.42	P31749	Y15748.1
extracellular signal-regulated kinase 1 (ERK1); mitogen-activated protein kinase 1 (MAP kinase 1; MAPK1); insulin- stimulated microtubule-associated protein-2 kinase; MNK1; PRKM3; ERT2; p44-MAPK	0.42	P27361	P21708
cytochrome P450 17 (CYP17); P450C17; CYPXVII; steroid 17-alpha-hydroxylase/17,20 lyase	0.42	NM_000102.2	X69816.1
ADP-ribosylation factor 5 (ARF5)	0.41	NM_001662.	NM_024149.1

GENE	Fold change	GenBank ID Human	GenBank ID Rat
rab12, ras related GTPase	0.41	-	M83676.
microsomal glutathione S-transferase (GST12; MGST1)	0.40	XM_048886.3	J03752
apolipoprotein A-I precursor (APO-AI)	0.38	X02162	M00001
presenilin 1 (PSNL1; PSEN1; PS1); S182 protein	0.38	XM_007441.1	D82363
amonipeptidase B	0.38	XM_087242.1	U61696
leukocyte common antigen-related tyrosine phosphatase (LAR)	0.38	-	U00477.1
NADPH-cytochrome P450 reductase (CPR); POR	0.37	S90469	NM_031576.1
protein kinase C delta type (PKC-delta)	0.36	NM_006254.1	M18330
proteasome delta subunit precursor; macropain delta; multicatalytic endopeptidase complex delta; proteasome subunit Y; proteasome subunit 5; PSMB6	0.36	X61971.1	NM_057099.1
sodium channel SCNB2, beta 2 subunit, brain	0.36	AAC05208.1	NM_012877.
retinoid X receptor alpha (RXR alpha; RXRA); NR2B1	0.35	XM_088424.1	NM_012805.1
PDGF-associated protein	0.35	U41745.1	U41744.1
Na+/K+ ATPase alpha 1 subunit	0.35	AAA51801.1	M28647
RalGDSB; GTP/GDP dissociation stimulator for a ras-related GTPase	0.34	-	NM_019250.1
interferon regulatory factor 1 (IRF1)	0.33	XM_034862.1	M34253
LIM domain protein CLP36, homologous to rat RIL	0.33	AJ310549.1	U23769.1
adenylate kinase 3	0.33	XM_016642.3	NM_013218.1
INOSITOL TRIPHOSPHATE RECEPTOR SUBTYPE 3	0.33	-	L06096.1
endothelin converting enzyme	0.33	Z35307.1	D29683
fibroblast ADP/ATP carrier protein; ADP/ATP translocase 2; adenine nucleotide translocator 2 (ANT2)	0.33	J02683	D12771
cytochrome c oxidase, subunit Va, mitochondrial	0.31	M22760.1	X15030
fatty acid-binding protein (intestinal; I-FABP; FABPI)	0.31	M18079	M18080.1
ornithine decarboxylase (ODC)	0.31	X16277	D11372.1
antigen peptide transporter 1	0.30	X57522	P36370
lipocortin 2	0.29	D00017.1	S73557
signal transducer CD24 precursor; heat stable antigen (HSA); nectadrin	0.28	P25063	U49062
cytoplasmic beta-actin (ACTB)	0.25	M10277.1	V01217
fructose-bisphosphate aldolase B (ALDOB); liver-type aldolase	0.24	XM_042788.1	M10149
granzyme M precursor (GZMM); MET-ASE; natural killer cell granular protease; RNK-MET-1	0.24	NM_005317.2	Q03238
scavenger receptor class B type I	0.24	-	AB002151.1
glutamyl aminopeptidase A	0.24	XM_003595.2	S73583
metalloendopeptidase meprin beta subunit	0.23	-	M88601.1
glutathione synthetase (GSH synthetase; GSH-S; GSS); glutathione synthase	0.23	U34683.1	L38615.1
cytochrome oxidase, subunit I, Sertoli cells	0.23	S79304	S79304
CamK I; calcium/calmodulin-dependent protein kinase type I + CaM-like protein kinase	0.23	Q14012	L24907
C-type natriuretic peptide precursor (CNP; NPPC)	0.22	NM_024409.1	D90219

GENE	Fold change	GenBank ID Human	GenBank ID Rat
neurotrophin 3 precursor (NTF3); neurotrophic factor; HDNF; nerve growth factor 2 (NGF2)	0.20	M37763.1	M34643
phospholipase C beta 3 (PLC-beta 3)	0.19	NM_000932.1	M99567
ATP synthase, subunit c, P2 gene	0.19	D13119.1	D13124
gelatinase A	0.19	NM_004530.1	U65656
glutathione S-transferase Ya subunit (GST YA); ligandin subunit 1 alpha	0.18	NM_000852.2	K01932
creatine kinase, ubiquitous, mitochondrial	0.18	XM_016524.4	X59737
fatty acid-binding protein (liver; L-FABP); Z-protein; squalene- & sterol-carrier protein (SCP); P14	0.18	NM_001443.1	M35991
cytochrome P-450 4F1, hepatic tumour	0.18	-	NM_019623.1
CamK II; calcium/calmodulin-dependent protein kinase brain type II beta	0.18	NM_001220.1	M16112
sodium-glucose cotransporter 1	0.16	P13866	U03120
fructose (glucose) transporter	0.16	AAB60641	D13871.1
urate transporter/channel	0.15	-	U67958
sodium/potassium-transporting ATPase beta 1 subunit (ATP1B1)	0.13	NM_001677.1	NM_013113.1
fatty acid amide hydrolase	0.12	U82535.1	U72497
proton-coupled dipeptide cotransporter	0.11	-	D50306.1
angiotensin converting enzyme (ACE; somatic; dipeptidyl carboxypeptidase I; kininase II	0.11	NM_000789.1	NM_012544.1
apolipoprotein A-IV precursor (APO-AIV)	0.10	XM_052144.2	P02651
ErbB3 EGF receptor-related proto-oncogene; HER3	0.08	M29366.1	NM_017218.2
Jun-B; c-jun related TF,	**	M29039.1	X54686
S-myc proto-oncogene; myc related,	**		M29069
C-est-I proto-oncogene; p54.	5	AF193068.1	X55787.1
Jun-D; c-jun related TF,	1.79	X56681.1	D26307(mouse)
NF-kappaβ Tf p105 subunit,	1.67	P19838	L26267.1
Nm23-M2; nucleoside diphosphate kinase B; metastasis reducing protein,	1.47		X68193.1 (mouse)
STAT 3 - signal transducer and activator of transcription 3,	1.16	NM_003150.1	NM_012747.1
CREB active TF,	1		M34356.1
New england deaconess TF,	1		U09229
Lim-2; embryonic motor neuron topographic organizer; homeobox protein LIM-2, and	1		L35572
NDK-B; nucleoside diphosphate kinase B ; metastasis reducing protein,	0.81		U29200.1
C-jun proto-oncogene; TF AP-1; RJG-9,	0.5	J04111.1	X17215.1

Symbols indicating fold changes in Table 2:

** : expressed in PP but not NPP, or in co-culture but not in Caco-2 cells.

* : expressed in co-culture but not in Caco-2 cells (only repeated once).

- :expressed in Caco-2 but not in co-culture.

Example 5

ATLAS array data on co-culture of human Caco-2 cells and Raji B-cells

In order to facilitate the routine study of M cell biology, there was a desire to establish a suitable and representative in-vitro model. In the work carried out by Kernéis *et al.* (Kerneis S, Caliot E, Stubbe H, Bogdanova A, Kraehenbuhl J, Pringault E (2000). Molecular studies of the intestinal mucosal barrier physiopathology using co-cultures of epithelial and immune cells: a technical update. Microbes Infect 2000 Jul;2 (9):1119-24), it was reported that Peyer's patch lymphocytes co-cultured with Caco-2 cells trigger the phenotypic conversion of enterocytes into cells that express morphological and functional M-cell properties. This work was further developed by Gullberg *et al.* (Gullberg E, Leonard M, Karlsson J, Hopkins AM, Brayden D, Baird AW, Artursson P. Expression of specific markers and particle transport in a new human intestinal M-cell model. Biochem Biophys Res Commun 2000 Dec 29; 279(3): 808-13) to create a simplified in vitro model of the human M-cell. Co-cultures of physically separated human intestinal epithelial Caco-2 cells and B-cell lymphoma Raji cells were established. The co-cultures were characterized under the criteria of morphology, integrity, expression of M-cell markers and cell adhesion molecules (CAMs), and altered particle transport. Using this construct, the epithelial cells were transformed to cells with an M-cell-like morphology and had altered expression of potential human M-cell markers (alkaline phosphatase down-regulation and Sialyl Lewis A antigen up-regulation). The expression of intercellular adhesion molecule-1 and vascular cell adhesion molecule was altered, and there was an increased binding of lectins wheat germ agglutinin and peanut agglutinin with a 40-fold increase in microparticle transport. The particle transport was size-dependent and could be inhibited at 4°C or by replacing the Raji B-cells with Jurkat T-cells. Thus the comparison of RNA isolated from co-cultured Caco2 cells to that isolated from normal Caco2 cells was designed to simulate a comparison of M cell RNA to normal gut enterocyte RNA.

Isolation of total RNA from Co-Cultured Caco-2 cells

Caco-2 cell culture

Caco-2 cells were cultured in Dulbecco's Modified Eagles Medium (DMEM), 4.5g/L glucose supplemented with 1% Mem, 10% FCS and 1% penicillin/streptomycin a t 37°C and

5% CO_2 in 95% relative humidity. Cells were grown and expended in Falcon culture flasks and passaged once they attained 100% confluence. Caco-2 cells were seeded on Transwell Clear filters (Costar, 12mm diameter, 3.0um pore size)) at a density of $5x10^5$ cells/cm2 and incubated in a 12 well culture plate with a medium change every second day. 1.0ml was added to the basolateral side and apical sides.

Raji cell culture

Raji B-lymphoma cells were cultured in RPMI 1640 Medium, with 1% (v/v) non-essential amino-acids, 10% FCS and 1% penicillin/streptomycin, 1% L-glutamine at 37°C and 5% CO2 in 95% relative humidity. Cells were grown in suspension in Falcon tissue culture flasks and passaged by dilution every 5-7 days.

Co-culture: day 14 (treating with Raji B-cells)

After 14 days of culturing Caco-2 monolayers, 15-20ml of Raji cells were removed from the T75 flask and placed in a 20ml universal. The cells were centrifuged at 1000 rpm for 3 min. Cells were re-suspended at a concentration of 1x106 cells/ml. 1ml of fresh complete DMEM was added to the apical and basolateral sides of the Caco-2 monolayer filters. 0.5 ml of $1x10^6$ Raji cells/ml cells was added to the basolateral side of the filters. For control filters (non co-culture) 0.5ml of Raji medium only was added to the basolateral side.

Isolation of Total RNA from co-cultured Caco-2 cells

After 4 days of co-culture the filters were rinsed in PBS. 0.5 ml of PBS was added to the apical side of each filter and the Caco-2 cells were scraped off the filter surface into suspension in the PBS. The cells from all the co-cultured Caco-2 filters were pooled, centrifuged at 1000 rpm for 3 min, the supernatant PBS was removed and the pellet was used for RNA extraction.

Analysis of mRNA expression

Total cellular RNA was extracted using an acid guanidinium thiocyanate-phenol-chloroform method. . RNA's integrity was confirmed by gel electrophoresis and ethidium bromide staining. mRNA was reverse transcribed in the presence of P^{32} dATP, and the transcribed cDNA was purified by chromatography before being hybridized over night to the array membrane. Membranes were exposed to x-ray film using an intensifying screen for 3 days and the mRNA expression levels were analyzed by scanning the films with a

densitometer. Expression levels were normalized relative to internal standards, and relative increases in mRNA levels in co-cultured cells versus monoculture controls were calculated. Two hybridization experiments were performed using mRNA from two separate cell harvests. Results from the two experiments were pooled, and a summary of the findings was tabulated in Tables 3(a)-3(f). The identified genes are from the following groups: oncogenes, tumor suppressor genes, genes involved in the cell cycle, ion channels and transport, stress response genes, modulators and effectors, genes involved in intracellular transduction, genes linked to apoptosis, DNA synthesis, repair & recombination, transcription factors, DNA binding proteins, receptors, cell surface antigens, genes involved in cell adhesion, growth factors, cytokines, chemokines and hormones.

In Table 3, genes which were found to be exclusively over-expressed in the co-culture and not in the control Caco-2 monolayer are represented by **. A single asterisk represents genes that also were expressed in the co-culture and not in the control Caco-2 monolayer. However, these particular genes have been distinguished from the genes labeled with two asterisks as they were not expressed in both hybridization experiments performed, and will require confirmation in the future by PCR so as to rule out false positives/negatives. Genes not expressed in the co-culture but expressed in the Caco-2 monolayer controls are indicated by a minus symbol, "-".

Table 3 a: Oncogenes, Tumor Suppressors, Cell Cycle Regulators

Gene	Fold change	GenBank ID
Myeloid cell nuclear differentiation antigen (MNDA)	*	M81750
G1/S-specific cyclin D1 (CCND1); cyclin parathyroid adenomatosis 1 (PRAD1); bcl-1 oncogene	*	X59798
cyclin-dependent kinase 4 inhibitor 2 (CDK4I; CDKN2); p16-INK4; multiple tumor suppressor 1 (MTS1)	*	L27211.1
cyclin-dependent kinase inhibitor 1C (CDKN1C); p57-KIP2	*	U22398
ezrin; cytovillin 2; villin 2 (VIL2)	1.69	X51521
proto-oncogene tyrosine-protein kinase kit; c-kit; mast/stem cell growth factor receptor precursor(SCFR); CD117 antigen	1.55	L04143.1
proliferating cell nucleolar antigen P120; NOL1	1.52	M32110
jun proto-oncogene; avian sarcoma virus 17 oncogene homolog; transcription factor AP-1	1.47	J04111
C-src proto-oncogene (SRC1)	1.35	X59932
CDC-like kinase 3 (CLK3)	1.35	L29220
cell division cycle protein 25 nucleotide exchange factor (CDC25)	1.34	M91815.1
prothymosin alpha (PROT-alpha; PTMA)	1.32	M26708
40S ribosomal protein S19 (RPS19)	1.31	M81757
avian myelocytomatosis viral oncogene homolog (MYC)	1.30	V00568
CDC-like kinase 1 (CLK1)	1.27	L29219.1
cyclin-dependent kinase 4 inhibitor 2D (CDKN2D); p19-INK4D	0.69	U49399.1
vascular endothelial growth factor receptor 1 (VEGFR1); tyrosine-protein kinase receptor flt + soluble VEGFR; tyrosine-protein kinase receptor SFLT	0.62	XM_039993.2
neogenin	-	U61262.1
webB2 receptor protein-tyrosine kinase; neu proto-oncogene; c-erbB2 + HER2 receptor	-	M11730.1
N-ras; transforming p21 protein	-	AAA60255

Table 3 b: Ion Channels, Modulators, Effectors

Gene	Fold change	GenBank ID
extracellular signal-regulated kinase 3 (ERK3); mitogen-activated protein kinase 6 (MAP kinase 6; MAPK6; PRKM6); p97-MAPK	**	X14798.1
40-kDa heat-shock protein 1 (HSP40); DNAJ protein homolog 1 (HDJ1; DNAJ1)	**	D49547
70-kDa heat shock protein 1 (HSP70.1; HSPA1)	**	M11717
glutaredoxin	**	X76648
tyrosine kinase receptor tie-1 precursor	*	AAB84296
ras-related protein RAB3B	*	NM_002867.1
macMARCKS; MARCKS-related protein (MRP); MLP	*	P49006
mitogen-activated protein kinase 3 (MAPK3; PRKM3);	*	P27361

Gene	Fold change	GenBank ID
MAPK1; extracellular signal-regulated kinase 1 (ERK); microtubule-associated protein 2 kinase; insulin-stimulated MAP2kinase		
mitgoen-activated protein kinase 9 (MAP kinase 9; MAPK9; PRKM9); c-jun N-terminal kinase 2 (JNK2); JNK55	*	NM_002752.1
60-kDa heat shock protein (HSP60); HSPD1; 60-kDa chaperonin; mitochondrial matrix protein P1 precursor; p60 lymphocyte protein; HUCHA60; GROEL	*	M22382.1
serine kinase	2.24	U09564.1
transferrin receptor (TFRC); CD71 antigen	1.80	M11507.1
Neurotrophic tyrosine kinase receptor-related 3: TKT percursor	1.63	U55017.1
phospholipase C (PLCL)	1.62	X14034.
cAMP-response element binding protein (CREB)	1.59	M27691.1
ephrin type-A receptor 1 precursor; tyrosine-protein kinase receptor eph	1.55	M18391
27-kDa heat-shock protein (HSP27); stress-responsive protein 27 (SRP27); estrogen-regulated 24-kDa protein; HSPB1	1.42	X54079.1
tyrosine kinase tnk1	1.42	XM_012654.3
ras-related protein RAB3A	1.38	XM_054457.2
janus kinase 3 (JAK3); leukocyte janus kinase (L-JAK)	1.33	XM_038595.3
dual-specificity mitogen-activated protein kinase kinase 1 (MAP kinase kinase 1; MAPKK 1; MKK1); extracellular signal-regulated kinase 1; ERK activator kinase 1	1.29	NM_002755.2
calcium/calmodulin-dependent protein kinase type IV catalytic subunit (CAMK IV); CAM kinase-GR	1.27	NM_001744.1
ras-related protein RAB5A	0.75	XM_053461.2
colon carcinoma kinase 4 precursor (CCK4) + transmembrane receptor PTK7	0.68	U33635.1
epithelial discoidin domain receptor 1 precursor (EDDR1; DDR1); cell adhesion kinase (CAK); TRKE; RTK6; protein tyrosine kinase 3A (PTK3A); neuroepithelial tyrosine kinase (NEP)	0.63	XM_004559.5
ras-related protein RAB6	0.27	M28212.1
cAMP-dependent protein kinase type I beta regulatory subunit (PRKAR1B)	0.23	M65066.1
tyrosine-protein kinase ack	-	CAC15525
T-lymphocyte maturation-associated protein MAL	-	P21145
orphan hormone nuclear receptor	-	U04897.1
LIM domain kinase 1 (LIMK-1)	-	P53667
protein kinase C alpha polypeptide (PKC-alpha; PKCA)	-	NM_002737.1
dual specificity mitogen-activated protein kinase kinase 3 (MAP kinase kinase 3; MAPKK3; MKK3); ERK activator kinase 3; MAPK/ERK kinase 3 (MEK3)	-	P46734
Yamaguchi sarcoma viral-related oncogene homolog; tyrosine –protein kinase lyn	-	M16038.1
protein-tyrosine phosphatase 1E	-	U12128.1

Table 3.c: Apoptosis, DNA Synthesis, Repair & Recombination

Gene	Fold change	GenBank ID
ubiquitin-conjugating enzyme E2 17-kDa (UBE2A); ubiquitin-protein ligase; ubiquitin carrier protein, HR6A	**	NM_003336.1
growth arrest & DNA-damage-inducible protein 153 (GADD153); DNA-damage-inducible transcript 3 (DDIT3); C/EBP homologous protein (CHOP)	**	S40706.1
growth factor receptor-bound protein 2 (GRB2); ASH protein	*	M96995.1
glutathione S-transferase A1 (GTH1; GSTA1); HA subunit 1; GST-epsilon	*	M21758.1
cytoplasmic dynein light chain 1 (HDLC1); protein inihibitor of neuronal nitric oxide synthase (PIN)	*	U32944.1
xeroderma pidmentosum group G complementing protein (XPG); X-ray repair-complementing defective repair in Chinese hamster cells 5 (XRCC5)	*	NM_021141.2
xeroderma pigmentosum group D complementing protein (XPD); X-ray repair-complementing defective repair in Chinese hamster cells 2 (XRCC2)	*	AF035587.1
RAD23 homolog A (RAD23A; hHR23A)	*	NM_005053.1
ataxia telangiectasia (ATM)	*	AAB38309
apoptosis regulator bcl-x	1.60	Z23115.1
caspase 9 percursor (CASP9); ICE-like apoptotic protease 6 (ICE-LAP6); apoptotic protease MCH6; apoptotic protease activating factor 3 (APAF3)	1.42	AB020979.1
CD40 receptor-associated factor 1 (CRAF1)	1.39	U21092.1
SL cytokine precursor; FMS-related tyrosine kinase 3 ligand (FLT3 ligand; FLT3LG)	1.35	NM_001459.1
cytochrome P450 reductase	1.33	AAD45961.1
X-ray repair complementing defective repair in Chinese hamster cells 1 (XRCC1)	1.25	M36089
Ku (p70/p80) subunit; ATP-dependent DNA helicase II 86-kDa subunit; lupus ku autoantigen protein; thyroid-lupus autoantigen (TLAA); CTC box binding factor 85-kDa subunit (CTCBF; CTC85); nuclear factor IV	0.74	X57500.1
caspace 10 precursor (CASP10); ICE-LIKE apoptotic protease 4 (ICE-LAP4); apoptotic protease MCH4; fas-associated death domain protein; interleukin 1 beta-converting enzyme 2 (FLICE2);	0.45	Q92851
inhibitor of apoptosis protein 2 (HIAP2; IAP2) + IAP homolog B; TNFR2-TRAF signaling complex protein 2; MIHB	-	Q13490
recA-like protein HsRad51; DNA repair protein RAD51 homolog	-	BAA02962.1
DNA damage repair & recombination protein 52 (RAD52)	-	B56529
DNA ligase III (LIG3); polydeoxyribonucleotide synthase	-	CAA59230.1

5

Table 3 d: Transcription Factors, DNA Binding Proteins

Gene	Fold change	GenBank ID
transcriptional activator hSNF2-alpha	**	D26155.1
early growth response protein 1 (EGR1); transcription factor ETR103; KROX24; zinc finger protein 225 (ZNF225); AT225	2.71	M62829.1
homeobox A1 protein (HOXA1); HOX1F	2.17	U10421.1
transcription factor NF-ATc	1.67	U08015.1
R kappa B DNA-binding protein	1.66	U08191.1
transcription initiation factor IID 31-kDa subunit (TFIID); TATA-box-binding protein-associated factor RNA polymerase II G 32-kDa subunit (TAFII32; TAF2G); TAFII31	1.57	M55654
homeobox protein hLim1; LHX1	1.51	NM_005568.1
helix-loop-helix protein HLH 1R21; DNA-binding protein inhibitor Id-3; HEIR-1	1.49	X69111.1
guanine nucleotide-binding protein G-s alpha subunit (GNAS); adenylate cyclase-stimulating G alpha protein	1.46	NP_000507.1
CCAAT-binding transcription factor subunit B (CBF-B); NF-Y protein subunit A (NF-YA); Hap2; CAAT-box DNA-binding protein subunit A	1.45	AAA40889.1
transcription factor LSF	1.37	B53771
homeobox 2.1 protein (HOX2A); HOXB5; HU1; HHO.C10	1.35	M92299.1
endothelial transcription factor GATA2	1.34	M68891.1
transcription factor Sp1 (TSFP1)	1.30	XM_028606.2
transcription factor ZFM1	0.62	G02919
zinc finger protein 161 (ZNFI61); putative transcription activator DB1	0.26	NP_009077.1
stem cell protein (SCL); T-cell leukemia/lymphoma-5 protein (TCL5); T-cell acute lymphocytic leukemia-1 protein (TAL1)	-	AAA36598.1
neural retina-specific leucine zipper protein (NRL)	-	NP_006168
MSX-1 homeobox protein; HOX7	-	P28360
basic transcription factor 62-kDa subunit (BTF2)	-	AAA58399.1
paired box homeotic protein (PAX8) isoforms 8A/8B + isoforms 8C/8D	-	BAB59039.1
brain-specific homeobox/POU domain protein 3A (brn-3A); RDC-1; octamer binding transcription factor 1 (OTF1)	-	AAA65605.1
transcription factor E2-alpha (E2A); immunoglobulin enhancer binding factor E12; transcription factor-3 (TCF3)	-	AAA61146.1
transcriptional enhancer factor (TEFI); protein GT-IIC; transcription factor 13 (TCF13)	-	P28347
thioredoxin perodxidase 2 (TDPX2); thioredoxin-dependent peroxide reductase 2; proliferation-associated gene (PAG); natural killer cell enhancing factor A (NKEFA)	-	Q06830

Table 3 e: Receptors, Cell Surface Antigens, Cell Adhesion

Gene	Fold change	GenBank ID
interleukin-2 receptor gamma subunit (IL-2R gamma; IL2RG); cytokine receptor common gamma chain precursor; p64	*	AAA59145.1
interferon gamma receptor (IFNGR)	*	NM_000416.1[
interleukin-1 receptor type I precursor (IL-1R1); IL-1R-alpha; p80; CDW121A antigen	*	M27492.1
neural-cadherin precursor (N-cadherin; NCAD); cadherin 2 (CDH2)	*	L34059
neural cell adhesion molecule L1 precursor (N-CAM L1); MIC5	*	M77640
integrin alpha 3 (ITGA3); galactoprotein B3 (GAPB3); very late antigen 3 alpha subunit (VLA3 alpha); CD49C antigen	*	M59911.1
leukocyte adhesion glycoprotein p150, 95 alpha subunit precursor; leukocyte adhesion receptor p150, 95; CD11C antigen; leu-M5; integrin alpha X (ITGAX)	*	M81695.1
integrin beta 4 (ITGB4); CD104 antigen	*	X51841.1
CD44 antigen precursor (CD44); phagocytic glycoprotein I (PGP1); HUTCH I; extracellular matrix receptor III (ECMR III); gp90 lymphocyte homing/adhesion receptor (LHR); hermes antigen; hyaluronate receptor; heparan sulfate proteoglycan; epican	1.51	XP_030326.1
glutamate receptor subunit epsilon 3 precursor (GRIN2C); N-methyl D-aspartate receptor subtype 2C (NMDAR2C; NR2C)	1.44	NP_000826.1
CD27L antigen receptor precursor; tumor necrosis factor receptor superfamily member 7 (TNFRSF7); T14	0.7	P26842
integrin alpha L (ITGAL); leukocyte adhesion glycoprotein alpha subunit precursor; leukocyte function-associated molecule 1 alpha chain (LFAI); CD11A antigen	0.45	P20701
interleukin 2 receptor alpha subunit precursor (IL-2 receptor alpha subunit; IL2RA); TAC antigen; CD25 antigen	0.41	P01589
CDW40 antigen; CD40L receptor precursor; nerve growth factor receptor-related B-lymphocyte activation molecule	0.35	CAA43045.1
granulocyte colony stimulating factor receptor precursor (GCSF-R); CD114 antigen	-	Q99062
low-affinity nerve growth factor receptor (NGF receptor; NGFR); GP80-LNGFR	-	AAB59544.1
neuromedin B receptor (NMBR); neuromedin-B-preferring bombesin receptor	-	NP_002502.1
granulocyte-macrophage colony-stimulating factor receptor alpha (GM-CSFR-alpha); CSW116 antigen	-	Q00941
platelet membrane glycoprotein IIIA precursor (GP3A); integrin beta 3 (ITGB3); CD61 antigen	-	P05106
integrin alpha 7B precursor (IGA7B)	-	CAA52348.1

Table 3 f: Growth Factors, Cytokines, Hormones

Gene	Fold change	GenBank ID
Interleukin-10 precursor (IL-10); cytokine synthesis inhibitory factor(CSIF)	**	M57627
Granulocyte-macrophage colony stimulaitng factor (GM-CSF); CSF2	*	AAA52578.1
FMLP-related receptor I (FMLPRII); RMLP-related receptor I (RMLPRI)	*	AAA58482.1
Glia maturation factor beta (GMF-beta)	*	P17774
Hepatoma-derived growth factor (HDGF)	*	P51858
Macrophage inflammatory protein 1 alpha precursor (MIP1-alpha); tonsillar lymphocyte LD78 alpha protein; G0S19-1 protein; PAT 464.2; SIS-beta; small inducible cytokine A3 (SCYA3)	*	P10147
Monocyte chemotactic protein 1 precursor (MCP1); monocyte chemotactic and activating factor (MCAF); monocyte secretory protein JE; monocyte chemoattractant protein 1; HC11; small inducible cytokine A2 (SYCA2).	*	P13500
Oncostatin M (OSM)	*	NP_065391.1
Renin-binding protein (RENBP; RNBP)		XP_013053.3
Calgranulin B (CAGB); migration inhibitory factor-related protein 14 (MRP14); leukocyte L1 complex heavy chain; S100 calcium binding protein A9 (S100A9)	1.49	B31848
Placenta growth factors 1+2 (PLGF1 + PLGF2)	1.42	CAA38698.1
Vascular endothelial growth factor precursor (VEGF); vascular permeability factor (VPF)	1.42	AAA35789.1
Hepatocyte growth factor activator (HGF activator)	1.40	BAA74450.1
Follistatin-related protein precursor	1.34	AAA66062.1
Hepatocyte growth factor-like protein; macrophage stimulating protein (MSP)	1.29	AAA59872.1
Interferon gamma precursor (IFN-gamma, IFNG); immune interferon	1.29	P01579
WSL protein + TRAMP + Apo-3 + death domain receptor 3 (DDR3)	0.69	AAB41432.1
Neurotrophin-4 (NT4)	0.68	AAA60154.1
Interleukin-13 precursor (IL-13); NC30	0.39	P35225
Small inducible cytokine A5 (SYCA5); regulated on activation normal T-cell-expressed & secreted protein precursor (RANTES); SIS delta	0.38	XP_035842.1
Estrogen sulfotransferase (STE; EST1)	-	CAA72079.1
Keratinocyte growth factor (KGF); fibroblast growth factor 7 (FGF7)	-	AAA63210.1
Endothelial-monocyte activiting polypeptide II (EMAP II)	-	AAA62202.1
Leukemia inhibitory factor precursor (LIF); differentiation-stimulating factor (D factor); melanoma derived LPL inhibitor (MLPLI); HILDA	-	B36282
Acidic fibroblast growth factor (AFGF) + heparin-binding growth factor 1 precursor (HBGF-1) + beta-endothelial cell growth factor (ECGF-beta)	-	AAA51672.1
Insulin-like growth factor-binding protein 3 precursor (IGF-binding protein 3; IGFBP3; IBP3)	-	P17936

Symbols (Fold Changes)

** : Expressed in PP but not NPP, or in Co-culture but not Caco2.
* : Expressed in Co-culture but no Caco2 (only repeated once)
- : Expressed in Caco2 but not in co-culture.

Immunity

The events of the cell cycle occur under normal circumstances in a fixed sequence. Traditionally, the cycle is divided into two stages: cell division and the interphase. Cell division or mitosis is followed by cytokinesis and together they constitute the 'M phase' of the cell cycle. The interphase is divided up into the S, G_1 and G_2 phases. Briefly, during the S phase, DNA is replicated in preparation for mitosis, while the intermediate G phases are transitional periods involved in protein synthesis and cell growth. Activation of regulatory genes that control and maintain a cell's proliferative state by intracellular signals (discussed below) stimulates proliferation of the cell and initiates cell growth. A number of genes involved in these processes were differentially expressed in the co-culture model (as estimated by relative mRNA abundance) and discussed below.

The epithelial cells of the gut play an important part of the innate and specific immunity. IEC's are considered to be in a continuous controlled state of "physiological" inflammation and active processes continually take place to ensure that the tone of immunosuppression is maintained (Mayer, 2000). These unique regulators appear to control the mucosal immune system's condition. These distinct factors govern the immune response, whether it's immune suppression/tolerance, inflammation or a systemic immune response. A clearer understanding of the immunoregulatory features involved in mucosal immunity is clearly desirable and may lead to new approaches in disease and drug therapy. Genes detected in the co-culture model that may be related to or are involved in immune function in GALT are discussed below.

The gamma subunit if IL-2 receptor plays a pivotal role in formation of the full-fledged IL-2 receptor (Di Santo *et at., 1995).* In an interesting study where infant rats were studied from pre- to post weaned life Masjedi et al. (1999) assessed alterations in expression and phenotype of cells in the gut-associated lymphoid tissue. At an age when the immune system is believed to be immature and functionally naive they discovered interleukin-2 receptor (IL-2R) expression peaked approximately four-fold at midweaning in Peyer's patches, compared with adult animals (day 70) suggesting that IL-2R expression is an adaptation to the host's environment. In a similar way, the presence of IL-2R specific for cells in the co-culture could be a direct result of the environment. The common gamma c

chain of the interleukin 2 receptor, gamma is also a component of the receptors for IL-4, 1L-7, and IL-9 and plays a critical role in lymphoid development through its participation in the receptors for IL-2, IL-4, IL-7, IL-9, and IL-15 (Di Santo *et al., 1995)*

Interferon-γ (IFN-γ) exhibits various properties including antigrowth activity in neoplastic and normal cells, and regulatory roles in immune responses (Tsuji *et al.,* 1998). Kjerrulf *et al.* (1997) found that in IFN-γ receptor knockout mice (IFN-$\gamma R^{-/-}$) reduced mucosal antibody responses and decreased Th1 and Th2 activity after oral immunization. The presence of IFN- γ receptor in the M cell co-culture model could possibly augment a cross-regulation between the two Th subsets in the gut mucosa. It is noteworthy that the ligand, IFN-γ, mRNA was increased in the co-culture that was supported further by the significant secretion of IFN-γ from co-culture monolayers.

The C-C chemokines macrophage inflammatory protein 1 (MIP1α) and monocyte chemotactic protein (MCP1) are synthesized and expressed by epithelial cells (Vainer *et al.,* 1998; Kolios *et al.,* 1999). The purpose of these chemokines expression in the co-culture model could be to function not only in leukocyte migration, but also as adhesins in the interaction between leukocytes and colonic epithelium. However, another C-C chemokine, RANTES, mRNA was observed to be reduced in the co-culture. The reasons for this are unclear. Perhaps, the chemoattractant activities of other chemokines such as IL-8, MIP1a and MCP1 are sufficient for the M cell and in the absence of T cells the need for RANTES is not required.

From a gene delivery perspective, a higher capacity for translation and protein synthesis in PP tissue indicates that PP tissue is a preferred tissue to which to deliver genes coding for DNA vaccines or antigens. Thus the proposed higher translational capacity of PP tissue has implications for gene delivery especially DNA vaccine delivery and correspondingly antigen expression and local presentation to the mucosal immune system in the gastrointestinal tract. The TF coding genes may be important in priming M cells or precursor cells to M cells to adopt M cell phenotype and/or to facilitate priming of M cells to give a better immune cell outcome.

M cell receptors identified in Table 3(e) above are of particular interest in that they can be used for vaccine and delivery.

In view of the foregoing, in the method of the invention for increasing the level of a protein in a PP cell, which comprises delivering a nucleic acid coding for a protein, the protein may be selected from the group consisting of an IL-2 receptor, a gamma c chain of an IL-2 receptor, intereron - γ, and a C-C chemokine.

Proliferation and Growth

Cyclin DI is a protein involved in regulation of the cell cycle. Over-expression of the protein is associated with abnormal growth or neoplasia. This protein is positively induced by the p42/p44 MAP kinases (Lavoie *et al.*, 1996). It would be interesting if the neoplasia seen in M cells resulted from activation of this protein considering the coincidental induction of the p44 MAP kinase (ERK1) below. The reduction in cyclin-dependent kinase 4 inhibitor 2D (CDKN2D) mRNA that normally inhibits cell cycle progression (Guan *et al.*, 1996) would insinuate a similar function in the proliferation of these 'M cells.'

In contrast, the induction of cell cycle inhibitors such as cyclin-dependent kinase inhibitor (CDKI) and cyclin-dependent kinase 4 inhibitor (CDK4J) would appear to be working to counterbalance proliferative stimuli present in the M cell.

PLC-L (phospholipase C-deleted in lung carcinoma) is a putative tumor suppressor gene. It is believed that irregular (in fact deletion) expression of the PLC-L gene contributes to the growth of human lung carcinoma (Kohno *et al.*, 1995). It is possible then that its upregulation in the M cell model is acting as a negative regulator of growth in the cells, counterbalancing the many proliferative signals present.

Growth factor receptor-bound protein 2, GRB2, involved in growth factor control of ras signalling (Lowenstein *et al.*, 1992).

The intracellular signaling pathways responsible for cell cycle arrest and establishment of differentiated cells along the gut axis remain largely unknown particularly in the case for the development of M cells and the FAE. ERK3/MAPK6 is expressed solely in the co-culture. Extracellular signal-regulated kinases-1 (ERK1) also known as the p44 mitogen-activated protein (MAP) kinase (p44mapk) is also induced specifically in the co-culture model. ERK1 and ERK3 are proline-directed serine/threonine kinases that are activated in response to a variety of extracellular signals, including growth factors, hormones and, neurotransmitters. These MAP kinases are key molecules involved in intracellular signal transduction, and are key regulators of cell proliferation in mammalian cells (Davis, 1995). Results indicate that elevated p42/p44 MAPK activities stimulate cell proliferation of intestinal cells, whereas low sustained levels of MAPK activities have correlated with cell cycle arrest and an increased expression of sucrase isomaltase (Aliaga *et al.*, 1999). It is tempting to speculate that the presence of ERK3 together with the other MAP kinases apart from their proliferative effects are in part responsible for a reduction in sucrase isomaltase, a characteristic effect in M cells.

Lying upstream in the ERK signal cascade the tyrosine/threonine protein kinase, MAPK kinase (MAPKK1) is implicated in the regulation of cell growth and differentiation through the activation of ERK. In addition it is interesting to note that MAPKK3 was deleted in the co-culture cells. MAPKK3 phosphorylates and activates p38 MAP kinase alpha and gamma isoforms (Enslen *et al.*, 1998). The induction of the MAPKK1 gene along with serine kinase coincides with the induction of ERK1, highlighting the ERK cascade as an important signalling cascade in M cell maintenance. It is interesting to note that ERK activation is responsible for terminal differentiation of components of the crypt-villus. (Taupin and Podolsky, 1999)

However, glia maturation factor-β (GMF-β) is potentially offsetting the ERK cascade effects. It is known to inhibit MAP kinases particularly ERK1 and ERK2 and yet promotes the p38 MAPK (Zaheer and Lim, 1996 and 1998).

Findings suggest that positive and negative regulation of MAPK activity are associated with loss of normal growth control and may be involved in carcinogenesis of colon cancers. Jun kinases such as JNK2 (MAP kinase 9) mediate signal transduction of pro-inflammatory cytokines and cellular stress (Uciechowski *et al.*, 1996).

CD40 is a receptor on the surface of B-lymphocytes, the activation of which plays critical role in B cell proliferation and differentiation. CRAF1, (CD40 receptor-associated factor 1) encodes a protein that interacts directly with CD40 receptor (Cheng *et al.*, 1995). Its upregulation in the co-culture is perhaps a main determinant of lymphoepithelial crosstalk as discussed above.

The c-myc gene is commonly amplified and over-expressed in many human tumors (Ryan and Birme, 1996). A member of the myc family of helix-loop-helix transcription factors, c-myc is integral in controlling cell growth and promotes cell proliferation and transformation by activating growth-promoting genes (Thompson, 1998). Prothymosin-α (PT-α) is a nuclear protein and its expression is associated with alterations in the proliferative state of cells and has been reported to be regulated by the c-myc gene in vitro. (Smith, 1995; Mon *et al.*, 1993). The increased activity of c-myc in this model is likely to result in the increase in RT-α mRNA.

PKC-α protein levels regulate certain pathways that lead to the expression of differentiation-dependent genes. In a series of antisense transfection experiments where PKC-α expression in CaCo-2 cells was almost completely deleted, enhanced proliferation and a marked decrease in differentiation was observed, as well as a more aggressive transformed phenotype (Scaglione-Sewell *et al.*, 1998). In a similar fashion, the lack of PKC-

α mRNA detected in the co-culture 'M cells' may underlie some of the phenotype changes featured.

Glutathione S-transferase A1 (GSTA1) is a member of a multigene family of detoxification and metabolizing enzymes. Induction of GST enzyme activity has been demonstrated to act as a potent anti-proliferative and differentiating agent in Caco-2 cells (Stein *et al.*, 1996) suggesting a similar role in the 'M cell.'

Transcription factor GATA-2 is thought to maintain and promote the proliferation of early haematopoietic progenitor cells.

The placenta growth factor (PLGF) is a member of the vascular enciotheial growth factor (VEGF) family of growth factors. In addition to PLGF, VEGF mRNA was enhanced in the co-culture cells. These growth factors play a crucial role in angiogenesis during development and/or repair (Andre *et al.*, 2000). The augmented transcription of their mRNA is consequently not a surprising find. However, hypoxia and energy depletion are known to induce angiogenesis by increasing VEGF, expression and so the possibility that the co-culture conditions are responsible for these genes induction cannot be ruled out rather than a deliberate mechanism of neogenesis in M cell formation. VEGF receptor 1 (VEGFR1); the receptor for VEGF and PLGF, mRNA is down-regulated and is possibly a consequence of desensitization of the receptor by VEGF and PLGF binding, initiating a reduction in the receptor's RNA.

Coinciding with the above actions, the absence of growth factors such as insulin-like growth factor-binding protein 3 (IGFBP3) and keratinocyte growth factor (KGF) may be modulating enterocytic cell proliferation and differentiation.

Caco-2 cells have been shown to express the type I IL-1R. (Varilek *et al.*, 1994) Il-1Rα binds IL-1 and mediates cell signalling particularly signalling involved in cell proliferation (French *et al.*, 1996). The expression of IL-1R can be enhanced by IFN-y (Varilek *et al.*, 1994). Therefore, the expression of IL-1R type 1 mRNA in the co-culture is interesting when considering the significant expression of IFN-1 expressed in supernatants of the co-culture model.

In view of the foregoing, in the method of the invention for increasing the level of a protein in a PP cell, which comprises delivering a nucleic acid coding for a protein, the protein may be selected from the group consisting of cyclin D1, PLC-L, GRB2, ERK3/MAPK6, ERK1, ERK3, JNK2, CD40, CRAF1, C-MYC, PT-α, IL-R, PKC-α, GSTA1, GATA-2, and PLGF.

Differentiation

Development of cells or differentiation is dictated by the expression of a cell's genes specific to that cell. This is a particularly important aspect with regards to M cells.

The cortical cytoskeleton not only provides structural support to the plasma membrane but also contributes to important dynamic processes such as endocytosis, exocytosis, and transmembrane signalling pathways. Ezrin, or villin 2, is an F-actin associated molecule and is concentrated in surface projections such as microvilli and membrane ruffles where they link the microfilaments to the membrane and has been reported to be in abundance during development and differentiation of the intestinal epithelium. It was reported that hepatocyte growth factor (HGF/SF) could stimulate the tyrosine phosphorylation of ezrin in a human colon epithelial cell line, which induced the ezrin associated membrane ruffling. It is interesting to note that both hepatocyte growth factor activator (HGF activator) and hepatocyte growth factor-like protein were both upregulated in the co-culture model and taken with the augmented ezrin mRNA the induction of these genes would appear to underlie the mechanism involved in the morphogenesis observed in M-cells.

These data demonstrate that the expression of the ezrin gene is being regulated at the level of mRNA due to effects incurred by the B-cells. It is particularly relevant considering the observations of villin diffusely displayed in M-cells.

One method of actin cytoskeletal reorganization is controlled by the LIMK-1 serine/threonine kinase, which acts by phosphorylating cofilin and subsequently Rac (as previously reported). However, LIMK-1 was deleted in the co-culture model and would appear to rule out the Rac-mediated mechanism of actin reorganization in the M cell model.

The cadherin family of cell adhesion molecules play important role in cell-cell adhesion during tissue differentiation. They have been reported to be linked to the actin cytoskeleton by catenins located in the cytoplasmic compartment of the cell. The specific expression of NCAD in the co-culture suggests a distinct gene involved in the cytoskeletal structure.

Previous reports have shown that neogenin is closely related to the human tumor suppressor molecule DCC (deleted in colorectal cancer) and together they constitute a subgroup of Ig superfamily proteins that have shown to be essential for terminal differentiation of specific cell types in the adult including the human colon. These parallels suggest that neogenin, like DCC, is functionally involved in the transition from cell

proliferation to terminal differentiation of specific cell types. Its absence in the co-culture model might represent a period of continued proliferation for the cells and allow a longer period of proliferation.

The helix-loop-helix (HLH) family of transcription factors has been shown by others to play a central role in the regulation of cell growth, differentiation and tumorigenesis. Of particular interest, when HLH 1R21 was over-expressed in mouse NIH3T3 cells, it induced a morphologically transformed phenotype.

Other genes associated with differentiation including Myeloid cell nuclear differentiation antigen (MNDA) and the LHX1 gene. The LHX1 gene is a member of the LIM/homeobox (Lhx) gene family. It has been shown that it codes for a transcriptional regulatory protein involved in the control of differentiation and development.

In view of the foregoing, in the method of the invention for increasing the level of a protein in a PP cell, which comprises delivering a nucleic acid coding for a protein, the protein may be selected from the group consisting of HGF activator, ezrin, NCAD, MNDA, and LHX1.

Adhesion

It is clearly evident that modification of the M cell apical surface is a determining factor in M cell apical membrane adherence, and thus, uptake and transport of macromolecules/microorganisms and targeting epitopes on the surface of M cells has been used to promote further adherence and uptake of particles in vaccinology. The specificity of these markers is not only useful for vaccine strategies but also represents targets for understanding adhesion and uptake of bacteria and viruses. Adhesion is not privy to the apical surface. Adhesion molecules on the basolateral surface of M cells, such as cadherin 2, neural cell adhesion molecule, integrin alpha 3, leukocyte adhesion glycoprotein p150, integrin beta 4 are understood to be involved in leukocyte migration and in the development/organization of lymphoid nodules in Peyer's patches. Genes expressed/induced in the co-culture can provide an insight into the mechanisms involved and are discussed below.

The tyrosine kinase receptor TIE 1 is normally located in vascular endothelial and haematopoietic cells and is largely involved in the proliferation and differentiation of miniature haematopoietic cells and would be an appropriate gene specific for M cells. In the brain, TIE

mRNA and protein is significantly elevated in lesions composed of abnormal vasculature called arteriovenous malformations (AVMs) and the surrounding vasculature. Like AVMs, the significant upregulation of TIE in M cells may indicate some ongoing neogenesis, and depending on the receptor's polarity could be of potential use in vaccine targeting.

The neuronal cell adhesion molecule L1 (NCAML1) is a transmembrane glycoprotein belonging to the immunoglobulin superfamily and is generally associated with development of the nervous system. As a potent promoter of neurite growth, it is allied with plastic changes. In nerve growth it interacts with the actin cytoskeleton via an ankyrin linkage and promotes specific distribution of F-actin. Such flexibility is ideal in the M cell scenario.

The integrin family consists of a series of related alpha beta heterodimers involved in a variety of cell-matrix and cell-cell adhesion functions. The $\alpha_3\beta_1$ integrin is a multiligand extracellular matrix receptor found on many cell types and can function as a receptor for fibronectin, laminin, and collagen. Phagocytosis of molecules by breast cells has also been reported to involve this adhesion molecule, thus, it would appear a suitable candidate as an adhesion target on M cells.

The leukocyte adhesion glycoprotein p150 (CD11C antigen), also a member of the integrin family, is involved in leukocyte sequestration via interaction of CD11/CD18 similar to that of ICAM-1.

In stratified epithelia β_4 integrin (CD1O4 antigen) has been shown to be important for proper differential expression and crucial for stable adhesion to die basement membrane through its ability to attach externally to laminin and internally to the keratin cytoskeleton. Interestingly, during human intestinal organogenesis receptors have been shown to occur. This integrin would appear to play an important role in epithelial cell-matrix interactions during development but particularly in M cell development.

CD44 is a major surface adhesion molecule involved in cell-cell and cell-matrix interactions and lymphocyte homing and activation. The observed enhanced expression suggests that this molecule is an important feature in the activities of M cells. A non-receptor tyrosine kinase, C-src protooncogene (SRC1) has been shown to cause overexpression of CD44 in the intestine. As well as its effects on proliferation, the enhanced activity of SRC1 seen in the M cell model would appear to have major effects on cell adhesion properties of the M cell. Hepatocyte growth factor activator (HGF activator) is a serine protease produced and normally secreted by the liver. It has been documented as stimulating reparative processes in intestinal epithelial cells and could be why its activity is enhanced in this model. However, stimulation of CD44 in colonic epithelial cells has been

reported to augment c-met, the HGF receptor. This in turn stimulates the "inside-out signalling causing an amplified expression of integrins that leads to an increase in vascular adhesion to the epithelium.

It has been reported that the glutamate receptor (NMDA) is generally associated with learning and memory, highly plastic processes in the brain. The high density of NMDA receptors reflects similar plastic changes seen in the co-culture model but would also act as a target epitope for drug delivery.

TKT is a tyrosine-kinase receptor related to TRK and is a member of cell adhesion kinase receptor family. Ephrin (type A) is a tyrosine kinase receptor that has been reported to be involved in neogenesis and tumor formation. Sp1 is a nuclear protein constitutively expressed and mediates basal promoter activity and is the main Vitamin-D receptor promoter in intestine. These are all potential target sites relevant to M cells.

Many of the receptors/cell surface antigen 'deleted' (not detectable) in the co-cultures could be putative negative markers of M cells. A good example is the laminin receptor $\alpha_7\beta_1$ integrin. Expression of the $\alpha_7\beta_1$ integtin correlates with human intestinal cell differentiation and could be used in a similar fashion that was applied with sucrase isomaltase and alkaline phosphatase.

In view of the foregoing, in the method of the invention for increasing the level of a protein in a PP cell, which comprises delivering a nucleic acid coding for a protein, the protein may be selected from the group consisting of cadherin 2, neural cell adhesion molecule, integrin alpha 3, leukocyte adhesion glycoprotein p150, integrin beta 4, TIE, NCAML1, $\alpha 3\beta 1$ integrin, CD11C antigen, CD104 antigen, CD44, NMDA, TKT, ephrin (type A), and Sp1.

Transport

The RAB proteins are reported to be regulators of polarized membrane traffic in epithelial cells. The RAB3B is localized to the apical pole very near the tight junctions between adjacent epithelial cells where it is reported to be a possible regulator of apical and/or jupctional protein traffic in epithelial tissues. RAB3B is highly homologous to a brain-specific RAB3 isoforin (RAB3A) that targets the presynaptic nerve terminal, where it is reported to regulate exocytosis.

In polarized cells, the small GTPase Rab5a is localized to the plasma membrane, clathrin-coated vesicles, and early endosomes and is a regulator of transport between the

plasma membrane and early endosomes. The decreased expression of RAB5a seen in the co-culture may deregulate the rate of endocytosis and/or vesicle fusion and could possibly release 'the brake' on vesicle trafficking.

RAB6 is another ras related protein also a regulator of intracellular transport in mammalian cells. It controls intra-Golgi transport, either acting as an inhibitor in anterograde transport or as a positive regulator of retrograde transport. Like RAB5a, the pronounced decrease seen in mRNA transcription could be a means of subverting transport regulation in epithelial cells and so optimize the process as observed in M cells.

Protein kinase C (PKC) and the actin cytoskeleton are critical effectors of membrane trafficking in mammalian cells. The F-actin cross-linking protein myristoylated alanine-rich C kinase substrate (MARCKS), a substrate for PKC, has been reported to be a component of the mechanism of endocytosis.

TIR or p71 plays a key role in the control of cell proliferation through the binding of transferrin, the major iron-carrier protein. Located on both apical and basolateral surfaces, the transferring receptor has the ability to internalize and recycle to the surface. Indeed experiments by Hughson and Hopkins (1990) demonstrate pathways from the apical and basolateral surfaces meet in an endosomal compartment. Furthermore, Shah and Shen (1994) discovered that the fungal metabolite brefeldin A (BFA) could relocate receptor distribution and enhance TfR mediated transcytosis. The increased expression of this mRNA in the M cell model suggests a potential delivery mechanism of protein drugs across the intestinal epithelium present in M cells that could be exploited.

In view of the foregoing, in the method of the invention for increasing the level of a protein in a PP cell, which comprises delivering a nucleic acid coding for a protein, the protein may be selected from the group consisting of a RAB protein, PKC, and TfR.

Signal transduction

In order for a cell to respond to extracellular signals, which cause it to alter gene expression or cellular function, it must involve the activation of a signal transduction cascade. There are many different types of signalling cascades, which can be unique to a specific type of stimulus. There are two main mechanisms by which these cascades transmit their signal, either through the regulation of enzymes, which produce second messenger molecules or through the regulation of protein phosphorylation. The activation of these cascades is usually mediated through specific cell surface or intracellular receptor proteins. The receptor

protein recognizes the incoming extracellular signal and responds accordingly, initiating a specific series of intracellular signal that direct the cell's behavior. A number of genes involved in intracellular signalling were upregulated or induced in the M cell model and are discussed below.

A member of the Janus family of tyrosine kinases, which are non-receptor protein kinases, Jak3 is involved in intracellular signalling mediated by cytokines and growth factors such as IL-2, IL-4, and IL-7. Jak3 has been reported to play a crucial role in Peyer's patch organogenesis. Mutant mice deficient in Jak3 presented defects in lymphocyte production and the absence of Peyer's patch structures. Its induced expression suggests a greater level of activity and possibly a major requirement underlying the M cell phenotype 'switch'.

The nuclear zinc-finger transcription factor, early growth response factor-I (EGR-1) is an immediate-early gene product expressed in response to diverse stimuli and is involved in growth, development, and differentiation. EGR-1 has been reported to function in growth regulation and suppression of cell transformation by transactivation of the TGFβ gene. TGFβ is capable of stimulating the synthesis of extracellular matrix proteins that can potentially stabilize epithelial cell contact with the substratum. In addition EGR-1 also plays a role in the immune response, regulating targets such as IL-2, CD44, ICAM-1, and TNF. Taken together the considerable induction of EGR-1 mRNA emphasizes the importance of this protein's involvement in M cell behavior.

CaM kinase IV (CAMK IV) is involved in Ca2+-dependent mechanism for regulating MAP kinase pathways. Many kinases activity has been observed to be enhanced in this model and so it is logical that CAMK IV expression is induced as a requirement to function.

The tyrosine kinase Tnk1 has been reported to be involved in signalling pathways involving development in adult tissues and in cells of the lymphohaematopoietic system.

Epithelial discoidin domain receptor 1 (EDDR1) mRNA was reduced in the co-culture. EDDR1 is a collagen receptor involved in controlling cellular responses to the extracellular matrix (ECM). The decrease in this gene would implicate it in the reorganization of the M cell in relation to the ECM.

cAMP-dependent protein kinase type I beta regulatory subunit (PRKAR1B) stimulates growth by modulating the signalling of camp via its regulation of cAMP-dependent protein kinase (PKA). PRKAR1B's reduction in the co-culture model may represent an inhibitory role in the cell's growth counterbalancing the proliferative signals.

In view of the foregoing, in the method of the invention for increasing the level of a protein in a PP cell, which comprises delivering a nucleic acid coding for a protein, the

protein may be selected from the group consisting of Jak 3, EGR-1, TNK1 and CAMK IV.

Protection and repair

Chaperones such as HSP40 and HSP 70 participate in many biological processes in which protein folding is involved. These include protein translocation, protein translation, protein assembly and disassembly, and protein degradation. It is understandable that such genes would be induced considering the evolving processes of a phenotype 'switch.' However heat shock protein production has been reported to be induced as a result of harsh changes in their environmental conditions such as stress, ishaemia or hypoxia resulting in protein damage. Therefore it cannot be ruled out that the induction of these genes is in fact a protective measure as a consequence of the adverse conditions in the co-culture.

HSP 60 has been observed in highly replicating cells e.g. short-living epithelial cells of the intestine. Involved in the import and refolding of nuclear-encoded proteins destined for the mitochondrial matrix.

The 27-kDa heat shock protein (HSP27) is expressed in a variety of tissues, including gut epithelia and in the absence of stress has been reported to regulate actin filament dynamics. Hsp27 induction in the M cell model like the other heat shock proteins (IISPs) may be active in development of resistance to stressful conditions. Activation of HSP27 can contribute to agonist-induced phosphorylation-modulated reorganization of the actin cytoskeleton and, in the case of stress activation, provides an actin-based adaptive response of cells to the new environmental conditions, and is ideal candidate for the plasticity seen in M cells.

Expression of receptors for fMLP on human phagocyles is well established, but there is conflicting evidence regarding the potential expression of fMLP receptors on other cells within the mucosa, particularly the epithelial cells. The reported observation of the receptor for the chemotactic peptide fMLP supports the notion of the intestinal epithelial cell as an early "sensor" of infection and inflammation. It has been reported that, fMLP, present in abundance in the lumen of the gut and that activation of fMLP receptors induces cytotoxic effects such as lysosomal release and superoxide generation. Thus, it would appear that their presence would be a defensive role in the event of infection of microorganisms.

Glutaredoxin (thioltransferase) is a small, heat-stable protein catalyzing glutathione-dependent disulfide oxdoreduction reactions in a coupled system with NADPH, GSH and glutathione reductase. It is important in regulating cell metabolism through the inactivation of

oxidated transcription factors thought to be important in cellular responses to oxidant stress. This modulation of transcription factors' binding activity has been demonstrated for a number of transcription factors, including NF-kB/Rel proteins, Fos and Jun proteins and nuclear factor I (NFI) family of transcription factors. The induction of such a gene would appear to provide a protective role and is particularly influential on a number of key transcription factors.

CREB has been implicated as having prominent role in protection. Over-expression of the gene was reported to reverse hypoxia elicited TNF induction. This infers that the increase in the cAMP responsive element binding protein (CREB) mRNA is possibly a protective response to conditions.

Inactive in cells under normal conditions, gadd153 expression is markedly induced in response to a variety of cellular stresses, including nutrient deprivation, DNA damage, and oxidative stress (e.g. free radicals) which normally leads to growth arrest. The arrest in growth is thought to allow critical repair processes to be carried out before any further cell cycling. It would appear that the gadd153 expression in the co-culture is for reparative purposes.

The excision repair proteins XPG and XPD have been reported to be involved in nucleotide repair. In addition, mRNA for ubiquitin-conjugating enzyme (likely to be involved in post-replication repair and induced mutagenesis, RAD23, and ataxia telangiectasia are also expressed in the co-culture. Their expression, coinciding with gadd153 suggests there is a high degree of impairment to genes in the M cell model.

Interleukin-13 (IL-13) is a potent anti-inflammatory cytokine and has been reported to have the same protective properties in inflammation as IL-4 through its ability to modulate and suppress pro-inflammatory cytokines. It is puzzling that in an environment with a high level of pro-inflammatory cytokines produced that IL-13 mRNA is in fact reduced. One possible explanation might be its anti-adhesion effect. It has been reported that IL-13 (secreted from lymhocytes) down regulated cell adhesion molecules in colonic epithelium and so the role of IL-13 in the co-cultured cells is modulating cell adhesion properties and not inflammation.

In view of the foregoing, in the method of the invention for increasing the level of a protein in a PP cell, which comprises delivering a nucleic acid coding for a protein, the protein may be selected from the group consisting of HSP40, HSP70, HSP60, HSO27, fMLP-related receptor, HSP27, glutaredoxin, CREB, gadd 153, XPG, XPD, ubiquitin, conjugating enzyme, RAD 23, and ataxia telengiectasia.

Apoptosis and programmed cell death

In programmed cell death, apoptosis is programmed in the sense that a genetically directed 'clock' selects a given time for the death of certain cells. It has been reported that it provides an important mechanism for the maintenance and renewal of cells in the gut and in development. However, for the epithelium to maintain its barrier functions, the level of apoptosis needs to be regulated, and this is 'checked' by several signal transduction systems. Toxic insult or lack of factors that maintain cell survival can also lead to apoptotic death of the cell.

It has been reported that over-expression of c-fos and c-jun (constituents of the AP-1 transcription factor) in the intestine correlates with programmed cell death and subsequent cellular regeneration. Other studies have demonstrated increases in both proximal jejunum and colon jun mRNA level coincide with a period of major changes in intestinal cell proliferation). The c-jun protein product involved in activation of AP-1, transcription is enhanced when it is phosphorylated by stress-activated protein kinases of which there are many in the M cell model.

As intestinal epithelial cells reach the villus apex they undergo apoptosis and, are shed and, in normal circumstances, caspases, a family of cysteine proteases, play a central role in initiating, amplifying, and executing apoptosis. The pattern of caspase activation in this process is not understood. It is interesting to note that the apoptosis regulator, bcl-x, and caspase 9 are induced in the co-culture. The bcl-x gene plays an important role in the regulation of programmed cell death (PCD), depending on its splice variant the bcl-x protein can accelerate apoptosis or delay/prevent programmed cell death (as previously reported). Bcl-x controls apoptosis mechanisms at points upstream of caspase activation. Perhaps, it is responsible for the marked induction of caspase-9. Caspase-9 is a caspase initiator. Once activated, it can proteolytically activate other caspases (including 3, 6 and 7), which in turn activate caspase-2 and 6 (as previously reported). Inhibitor of apoptosis protein 2 (HIAP2) binds to and inhibits caspase-3. Its expression is a mechanism of regulating cell death depending on the particular cellular or environmental signals. Therefore, its absence in the co-culture cells and the increased activity of caspase-9 allows caspase-3 unchecked pro-apoptotic activity.

The death domain receptor 3 (DDR3) member of the TNFR family can induce apotosis as previously reported. Its mRNA expression is also reduced in the co-culture model.

In view of the foregoing, in the method of the invention for increasing the level of a protein in a PP cell, which comprises delivering a nucleic acid coding for a protein, the protein may be selected from the group selected from: bcl-x and capase-9 and more generally in view of the foregoing may be selected from the group consisting of

cyclin D1, PLC-L, GRB2, ERK3/MAPK6, ERK1, ERK3, JNK2, CD40, CRAF1, C-MYC, PT-α, IL-R ,CD40, C-MYC, PKC-α, GSTA1, GATA-2, PLGF, ezrin, HGF activator, hepatocyte growth factor-like protein, NCAD, MNDA, LHX1, TIE-1, NCAML1, CD104, CD44, SRC1, NMDA, TKT, ephrin (type A), Sp1, RAB proteins, PKC, TIR, Jak3, EGR-1, TNK1, CAMK IV, HSP40, HSP70, HSP60, HSO27,fMLP-related receptor, HSP27, glutaredoxin, CREB, gadd153, XPG, XPD, ubiqitin- conjugating enzyme, RAD23, cadherin 2, neural cell adhesion molecule, integrin alpha 3, leukocyte adhesion glycoprotein p150, integrin beta 4, TIE, NCAML1, α3β1 integrin, CD11C antigen, CD104 antigen, CD44, NMDA, TKT, ephrin (type A), and Sp1, a RAB protein, PKC, and TfR, bcl-x and capase-9

Example 6

Targeted Gene delivery

Delivery of genes, gene fragments, oligonucleotides or other nucleotide fragments or analogues of the present invention to a living organism can be accomplished by methods currently available in the prior art. For example, various recombinant viruses have been used for the oral delivery of genes, such as adenovirus, retrovirus, adeno-associated virus, vaccinia virus, lenti-virus and plant-derived viruses, wherein the viral genome is replaced with an expression vector for the gene of interest. . *See*, David T. Page and Sally Cudmore (2001). Innovations in oral gene delivery: challenges and potentials. *Drug Discovery Today,* Vol. 6, No. 2, pp 92–101. Viral mimetic particles such as virosomes and various types of polymers and liposomes, such as cationic and fusogenic, are also employed for gene delivery. See, U.S. Patent Nos. 4885172, 5047245, 5171578, 5059421, 5399331, 5204112, 1252263, 5376452, 5552155, 6120797, 6087325, 6143716. Examples of polymers are PLGA, PLA co-polymers, chitosan, and fumaric acid/sebacic acid co-polymers. For these systems, the polymer or liposome is formed from component parts in a solution of the gene expression vector, thus encapsulating the genes when particles are formed. Cationic lipids such as DOTAP and polyethylenimine are commonly used whereby the gene expression vector is complexed with and protected by the lipids. (See, Ogris M. *et al.* (2001). DNA/polyethylenimine transfection particles: Influence of ligands, polymer size, and pegylation on internalization and gene expression. *AAPS PharmSci, 3 (3),* article 21).

Agents such as protamine are used to condense DNA, which due to the reduction in size of the DNA particles are more easily taken up by cells. Recombinant live bacteria (e.g. *Shigella* spp, *Salmonella* spp.) have also been exploited for gene delivery to the gut. Oral bioavailability enhancers, (e.g. sodium caprate, Elan's PROMDAS technology) could be used to increase uptake of a gene or encapsulated gene formulation.

In all cases the delivery systems can be targeted with various ligands on the surface of the particles in order to enhance binding to specific cells type and/or to enhance uptake. These ligands could be peptides, proteins, antibodies, peptidomimetics, and lipids that recognize or are being recognized by specific sites/receptors on the cell surface (Maruyama K. (2000). *In vivo* Targeting by Liposomes. *Biol. Pharm. Bull., 23(7), 791-799*).

The targeting ligands may be peptide based, peptidomimetic based, antibody based, single chain antibody based, small organic molecule based. The targeting ligands may also be natural substrates for such receptors, transporters or other cell surface molecules found on the surface of M cells or other cell types found in Peyer's patch. The targeting ligands may be engineered so as to be genetically expressed on the surface of viruses, bacteriophages, virosomes, bacteria or other organisms, which can be utilized for vaccine delivery in the gut. Furthermore the targeting ligands can be presented either as direct conjugates to antigens, or on the surface of drug-loaded particulates such as liposomes, PLGA particles, other particulates and at the same time retain recognition by and interaction with the receptors, transporters or other cell surface molecules found on the surface of M cells and / or other cells of Peyer's patch tissue.

Examples of peptides that target the gastro-intestinal tract, in particular, membrane translocating peptides useful for vaccine delivery to M cells along with M cell specific targeting ligands are described in Table 4.

Further, targeting ligands can be genetically engineered into the surface coats of viruses, bacteriophages or bacteria, conjugated directly to antigens conjugated to the lipids in liposomes by covalent methods or streptavidin-biotin linkages, or coated onto the surface of polymers after particle formation (Torchilin V.P. *et al.* (2001) *Proc. Natl. Acad. Sci. USA*, Vol. 98, Issue 15, 8786-8791, July 17.

TAT peptide on the surface of the liposomes affords their efficient delivery even at low temperature and in the presence of metabolic inhibitors; Lestini *et al.* (2002). Surface modification of liposomes for selective cell targeting in cardiovascular drug delivery. *J. Controlled Release, 78, 235-247;* Dokka S. *et al.* (1997) Cellular delivery of oligonucleotides by synthetic import peptide carrier. *Pharm. Res., vol. 14, No. 12, 1759-1764*); Wu Y *et al.*

(2000). Gene transfer facilitated by a cellular targeting molecule, retrovirus protein σ 1. *Gene Therapy, 7, 61-69*).

When the delivery of the gene to M cells in the gut is designed to prime or boost the immune system, the genes can be co-delivered/co-encapsulated with adjuvants (e.g. MF59, alum, saponin, QS21, MPL, bacterial toxins such as Lt, CT or mutants there-of, CPG motif nucleotides). Immune response could be boosted at a later stage by methods such as subcutaneous administration of an adjuvant.

In some cases it may be desired to shut off expression of certain genes, so as to enhance the adoption by enterocytes of an M cell phenotype. This can be achieved by the delivery, by methods outlined above, of antisense oligonucleotides, ribozyme, or RNA-interference molecules specific to the gene of interest.

Table 4

Peptides that Target to and/or Enhance Uptake Across the GIT

SEQ ID. NO:	PEPTIDE SEQUENCES
SEQ. ID NO:	ADDFMGCMLTLPTSLGGEGSPYNYYDTHEANGPH
SEQ. ID NO:	TPTTTATVVGTTGPVDLSSLHLLRHPCREF
SEQ. ID NO:	MSPDHQYALQSSPVLPCCRPLLVDSDYIHS
SEQ. ID NO:	RGYGRLAESCCVNRCIRTVGGCGNSPASDILSAT
SEQ. ID NO:	STPGRGSGRDTGANNPADTPYANPSHRDTILSLDPSLL
SEQ. ID NO:	RQHLVVRDLHGPRFRDTNTGVAGTFSPPVSVADTHRTPD
SEQ. ID NO:	SFSNLTAGDEEDDHFSGGRFNHANLTSRSHNRGQLASSA
SEQ. ID NO:	RQSVLDSWGGKTSVTGLSERYYASHSHTSAPTPHYASHS
SEQ. ID NO:	RQWVGDRDAGEGNTWVDEKYSRDANVISYRSHNHASQGTL
SEQ. ID NO:	RASDCDVECNLRWVEDVGGVWYAKTVSRMLSTT
SEQ. ID NO:	RQSAGFLGFAPTNIDDTSFNAGCGDTLAIPCRHRSSLISPARPP
SEQ. ID NO:	RSGAYESPDGRGGRSYVGGGGGCGNIGRKHNLWGLRTASPACWD
SEQ. ID NO:	SPRSFWPVVSRHESFGISNYLGCGYRTCISGTMTKSSPIYPRHS
SEQ. ID NO:	SSSSDWGGVPGKVVRERFKGRGCGISITSVLTGKPNPCPEPKAA
SEQ. ID NO:	RVGQCTDSDVRRPWARSCAHQGCGAGTRNSHGCITRPLRQASAH
SEQ. ID NO:	SHSGGMNRAYGDVFRELRDRWNATSHHTRPTPQLPRGPN
SEQ. ID NO:	SPCGGSWGRFMQGGLFGGRTDGCGAHRNRTSASLEPPSSDY
SEQ. ID NO:	RGAADQRRGWSENLGLPRVGWDAIAHNSYTFTSRRPRPP
SEQ. ID NO:	SGGEVSSWGRVNDLCARVSWTGCGTARSARTDNKGFLPKHSSLR
SEQ. ID NO:	SDSDGDHYGLRGGVRCSLRDRGCGLALSTVHAGPPSFYPKLSSP
SEQ. ID NO:	RSLGNYGVTGTVDVTVLPMPGHANHLGVSSASSSDPPRR
SEQ. ID NO:	RTTTAKGCLLGSFGVLSGCSFTPTSPPPHLGYPPHSVN
SEQ. ID NO:	SPKLSSVGVMTKVTELPTEGPNAIS IPISATLGPRNPLR
SEQ. ID NO:	RWCGAELCNSVTKKFRPGWRDHANPSTHHRTPPPSQSSP
SEQ. ID NO:	RWCGADDPCGASRWRGGNSLFGCGLRCSAAQSTPSGRIHSTSTS
SEQ. ID NO:	SKSGEGGDSSRGETGWARVRSHAMTAGRFRWYNQLPSDR
SEQ. ID NO:	RSSANNCEWKSDWMRRA.CIARYANSSGPARAVDTKAAP
SEQ. ID NO:	SKWSWSSRWGSPQDKVEKTRAGCGGSPSSTNCHPYTFAPPPQAG
SEQ. ID NO:	SGFWEFSRGLWDGENRKSVRSGCGFRGSSAQGPCPVTPATIDKH
SEQ. ID NO:	SESGRCRSVSRWMTTWQTQKGGCGSNVSRGSPLDPSHQTGHATT
SEQ. ID NO:	REWRFAGPPLDLWAGPSLPSFNASSHPRALRTYWSQRPR
SEQ. ID NO:	RMEDIKNSGWRDSCRWGDLRPGCGSRQWYPSNMRSSRDYPAGGH
SEQ. ID NO:	SHPWYRHWNHGDFSGSGQSRHTPPESPHPGRPNATI
SEQ. ID NO:	RYKHDIGCDAGVDKKSSSVRGGCGAHSSPPRAGRGPRGTMVSRL
SEQ. ID NO:	SQGSKQCMQYRTGRLTVGSEYGCGMNPARHATPAYPARLLPRYR
SEQ. ID NO:	SGRTTSEISGLWGWGDDRSGYGWGNTLRPNYIPYRQATNRHRYT
SEQ. ID NO:	RWNWTVLPATGGHYWTRSTDYHAINNHRPSIPHQHPTPI
SEQ. ID NO:	SWSSWNWSSKTTRLGDRATREGCGPSQSDGCPYNGRLTTVKPRT
SEQ. ID NO:	SGSLNAWQPRSWVGGAFRSHANNNLNPKPTMVTRHPT
SEQ. ID NO:	RYSGLSPRDNGPACSQEATLEGCGAQRLMSTRRKGRNSRPGWTL
SEQ. ID NO:	SVGNDKTSRPVSFYGRVSDLWNASLMPKRTPSSKRHDDG
SEQ. ID NO:	TNAKHSSHNRRLRTR
SEQ. ID NO:	SDNAKEPGDYNCCGNGNSTG
SEQ. ID NO:	RTRLRRNHSSHKANT

SEQ ID. NO:	PEPTIDE SEQUENCES
SEQ. ID NO:	GPHRRGRPNSRRSSKT
SEQ. ID NO	GTSNGNGCCNYDGP
	Peyers patch and/or M cell specific targeting ligands:
SEQ. ID NO:	ATPPPWLLRTAP
SEQ. ID NO:	DGSIHKRNIMPL
SEQ. ID NO:	DYDSLSWRSTLH
SEQ. ID NO:	GEPTTDMRWRNP
SEQ. ID NO:	GLWPWNPVTVLP
SEQ. ID NO:	HMLNDPTPPPYW
SEQ. ID NO:	KPAYTHEYRWLA
SEQ. ID NO:	LETTCASLCYPS
SEQ. ID NO:	LGTDWHSVSYTL
SEQ. ID NO:	LGTLNAGVPGFP
SEQ. ID NO:	LTHSKNPVFLST
SEQ. ID NO:	LVPTTHRHWPVT
SEQ. ID NO:	LVSNARGFNNLS
SEQ. ID NO:	NTRIPEPIRFYM
SEQ. ID NO:	NVYTFHSMSPMP
SEQ. ID NO:	QHTTLTSHPRQY
SEQ. ID NO:	SDFSDTMPHRPS
SEQ. ID NO:	SIDTIQILSLRS
SEQ. ID NO:	SISWASQPPYSL
SEQ. ID NO:	SMVKFPRPLDSR
SEQ. ID NO:	SPTLGASVAQTN
SEQ. ID NO:	TMSPNVYYTAFG
SEQ. ID NO:	TQIPSRPQTPSQ
SEQ. ID NO:	VCSNMYFSCRLS
SEQ. ID NO:	VPPHPMTYSCQY
SEQ. ID NO:	VPRLEATMVPDI
SEQ. ID NO:	VPTKPELPVNFT
SEQ. ID NO:	WSSDLPQPASTY
SEQ. ID NO:	YITPYAHLRGGN
SEQ. ID NO:	NVYTDNTLSPTP
SEQ. ID NO:	LETTAASLCYPS
SEQ. ID NO:	SPYCLSACTTEL
SEQ. ID NO:	LETTCASLCYPS
SEQ. ID NO:	VPPHPMTYSCQY
SEQ. ID NO:	VPPHPMTYSAQY
SEQ. ID NO:	VPPHPMTYSSQY
SEQ. ID NO:	YQCSYTMPHPPV
SEQ. ID NO:	VCSNMYFSCRLS
SEQ. ID NO:	VSSNMYFSSRLS
SEQ. ID NO:	DYDSLSWRSTLHGGHESSH
SEQ. ID NO:	GNPTSTMRW
SEQ. ID NO:	PWNSATVL
SEQ. ID NO:	NDPTAPPY

SEQ ID. NO:	PEPTIDE SEQUENCES
	Membrane Translocating Peptides: (underline denotes cyclization)
SEQ. ID NO:	KKAAAVLLPVLLAAP FITC-LC
SEQ. ID NO:	KKKAAAVLLPVLLAAP
SEQ. ID NO:	KKAAAVLLPVLLAAPREDL
SEQ. ID NO:	KKCAAVLLPVLLAAPC
SEQ. ID NO:	CAAVLLPVLLAAC
SEQ. ID NO:	KKCAAVLLPVLLAC
SEQ. ID NO:	CAAVLLPVLLC
SEQ. ID NO:	CAAVLLPVLC
SEQ. ID NO:	CAVLLPVLLAAPC
SEQ. ID NO:	CVLLPVLLAAPC
SEQ. ID NO:	CLLPVLLAAPC
SEQ. ID NO:	CLPVLLAAPC
SEQ. ID NO:	AAVLLPVLLAAP
SEQ. ID NO:	AAVLLPVLLAA
SEQ. ID NO:	KKAAVLLPVLLA
SEQ. ID NO:	AAVLLPVLL
SEQ. ID NO:	AAVLLPVL
SEQ. ID NO:	AVLLPVLLAAP
SEQ. ID NO:	VLLPVLLAAP
SEQ. ID NO:	LLPVLLAAP
SEQ. ID NO:	LPVLLAAP
SEQ. ID NO:	AAVLLPVLLAAKKKRKA
SEQ. ID NO:	KKKRKAAAAVLLPVLLA

Example 7

Use of bacterial coatings to convert enterocytes to M cells

Might be nice to have some type of claim capturing the concept from this section Use of bacterial coatings on PLGA particles, co-administered bacterial particles or pro-biotic yogurts as adjuvants for oral vaccination with PLGA particles. The invention is based on converting enterocytes to M cells by using specific bacteria in advance of, or along with the oral vaccine particle of interest. In doing so the capability of absorbing particles through M cells will be increased. This idea is not based on targeting but on the ability of live bacteria or active bacterial components to stimulate cytokine production in Peyer's patches, thus, enabling enterocyte-M cell conversion. As a result, an invention disclosed herein is a method of promoting enterocyte-M cell conversion, said method comprising orally administering an antigen, antigenic composition, or antigen-carrying particle to a person and either simultaneously with, or prior to, said administration, also orally administering a

bacteria, or pro-biotic yogurts, or bacterial component to said person.

All references cited herein are incorporated herein by reference in their entireties.

Table 5

Miscellaneous GenBank Accession Numbers

Human Serum Albumin	NM_000477.3
Calreticulin	M84739

Dates for GenBank records

To the extent the date of a GenBank record, rather than its version number, is relevant for purposes of incorporation by reference, the date of the record is the filing date of this application with the following exceptions:

Table 2: Rat genes

3/27/02 D83697 through M10149

3/28/02 Q03238 through NM_017218.2

Tables 3: Human genes with a fold change of 0.5 or less

4/02/02

Table 2 Human genes with a fold change of 0.5 or less

4/02/02 U76376.1 through XM_087242.1

4/03/02 S90469 through M29366.1

The records specified for 3/27/02, 3/28/02, 4/02/02, and 4/03/02, do not include those

of GenBank IDs: Q07912, P21145, P46734, Q92851, Q13490, NP_006168, P28360, P28347, Q06830, P20701, P01589, P05106, P35225, P17936, S18408, P17074, P10661, P35426, P09456, P22791, Q06486, P21708, Q03238, P10644, P54868, P10398, P48730, P31749, P27361, P25063, Q14012, P13866

5

CLAIMS

1. A method of increasing the levels of a protein in a Peyer's patch cell, said method comprising delivering to said cell a nucleic acid coding for a protein, wherein absent said increase, the levels of said protein or its mRNA is greater than in a non-Peyer's patch cell.

2. The method of Claim 1 wherein the protein is a transcription factor or a protein that activates a transcription factor.

3. The method of Claim 2 wherein the transcription factor or a protein that activates a transcription factor is selected from the group consisting of Jun-B; c-jun related TF, Jun-D; c-jun related TF, STAT 3 - signal transducer and activator of transcription 3, NF-kappaβ Tf p105 subunit, , S-myc proto-oncogene; myc related, Nm23-M2; nucleoside diphosphate kinase B; metastasis reducing protein, and C-est-I proto-oncogene; p54.

4. The method of Claim 1 wherein the protein is a receptor, or cell surface antigen,

5. The method of Claim 4 wherein the protein is a receptor or a transporter.

6. The method of Claim 1 wherein the protein is selected from the group consisting of nucleoside diphosphate kinases and member of the 14-3-3 family.

7. The method of Claim 1 wherein the protein is coded for by a gene with an expression Fold Change denoted by a **, *, or number greater than 2.00 in Tables 2 or 3.

8. The method of Claim 1 wherein the nucleic acid coding for at least 2 proteins is delivered, each of said proteins coded for by a gene with an expression Fold Change denoted by a **, *, or number greater than 2.00 in Tables 2 or 3.

9. The method of Claim 1 wherein the cell to which the nucleic acid is delivered is a human cell.

10. The method of Claim 9 wherein the cell is in a Peyer's patch in a human and the nucleic acid is delivered by the oral route.

11. The method of Claim 9 wherein the cell is not within the body of a human.

12. The method of Claim 1 wherein the cell to which the nucleic acid is delivered is a rat cell.

13. The method of Claim 1 wherein a nucleic acid coding for a tumor antigen or foreign peptide is also delivered to the Peyer's patch cell.

14. The method of Claim 13 wherein the cell to which the nucleic acid is delivered is a human cell.

15. A method of decreasing the levels of a protein in a Peyer's patch cell, said method comprising delivering to said cell an anti-sense nucleic acid molecule, a ribozyme nucleic acid molecule, an RNA interference nucleic acid molecule (RNAi), said anti-sense molecule, ribozyme or RNAi nucleic acid being complementary to a sequence of at least 10 nucleotides of the mRNA for said protein, wherein absent said anti-sense molecule, ribozyme or RNAi nucleic acid, the levels of said protein or its mRNA is less than in a non-Peyer's patch cell.

16. The method of Claim 15 wherein the anti-sense nucleic acid, a ribozyme nucleic acid molecule, an RNA interference nucleic acid molecule is complementary to a sequence of at least 15 nucleotides of the mRNA of the protein.

17. The method of Claim 16 wherein the anti-sense nucleic acid, a ribozyme nucleic acid molecule, an RNA interference nucleic acid molecule is complementary to a sequence of at least 30 nucleotides of the mRNA of the protein.

18. The method of Claim 15 wherein the protein is coded for by a gene with an expression Fold Change denoted by a "-", or a number less that 0.5 in Tables 2 or 3.

19. The method of Claim 15 comprising delivering to said cell anti-sense nucleic acid molecules, ribozyme nucleic acid molecules, RNA interference nucleic acid molecules, said anti-sense, ribozyme or RNAi nucleic acid being complementary to a sequence of at least 10 nucleotides of the mRNA for at least 5 different protein a, wherein absent said anti-sense, ribozyme or RNAi nucleic acid molecule, the levels of each of said proteins or its mRNA is less than in a non-Peyer's patch cell.

20. A method of decreasing the levels of a protein in a Peyer's patch cell, said method comprising delivering to said cell an anti-sense nucleic acid molecule, a ribozyme nucleic acid molecule, an RNA interference nucleic acid molecule said anti-sense, ribozyme or RNAi nucleic acid forming a double-stranded molecule with part or all of the mRNA for said protein, wherein absent said anti-sense, ribozyme or RNAi nucleic acid molecule, the levels of said protein or its mRNA is less than in a non-Peyer's patch cell.

21. A method of Claims 1, 13, or 15 in which the Peyer's patch cell is an M cell.

22. A human cell to which the method of Claims 1 has been applied, or the progeny of said human cell.

23. A human cell to which the method of Claim 13 has been applied, or the progeny of said human cell.

24. A human cell to which the method of Claim 15 has been applied, or the

progeny of said human cell.

25. A human cell to which the method of Claims 1 has been applied, or the progeny of said human cell.

26. A human cell to which the method of Claim 13 has been applied, or the progeny of said human cell.

27. A human cell to which the method of Claim 15 has been applied, or the progeny of said human cell.

28. A method for enhancing transport of a drug through the gastrointestinal tract, said method comprising orally administering said drug in a composition that comprises a transport-enhancing protein, said transport-enhancing protein selected from the group consisting of human serum albumin (HSA), clusterin, T-cell surface glycoprotein CD5 precursor, HSP84, and Ca2+pla2, or a homolog that has at least 80% amino acid identity with said transport-enhancing protein over a length of said transport-enhancing protein identical to the homolog.

29. A method of Claim 28 wherein the homolog has at least 90% amino acid with the transport-enhancing protein over a length of the transport-enhancing protein identical to the homolog.

30. A method of Claim 28 wherein the transport-enhancing protein is selected from the group consisting of human serum albumin (HSA), clusterin, T-cell surface glycoprotein CD5 precursor, HSP84, and Ca2+pla2.

31. A method to facilitate intracellular trafficking of an antigen that has been orally delivered by itself or as part of a composition or particle, said method comprising administering a protein selected from the group consisting of calreticulin, rab family proteins and ribosomal proteins.

32. A chimeric protein comprising the amino acid sequence for calreticulin, rab family proteins and ribosomal proteins and the amino acid sequence for a second polypeptide.

33. A method of administering a polypeptide, where said polypeptide is part of a chimeric protein of Claim 32, and wherein said chimeric protein is orally administered.

34. A method of delivering a vaccine to a target cell, said method comprising utilizing as the target cell a Peyer's patch cell in which a normally upregulated protein or mRNA is further upregulated.

35. A method of Claim 34 wherein the Peyer's patch cell is an M Cell.

36. A method of Claim 1 wherein the protein is selected from the group consisting

of clusterin, T-cell surface glcoprotein CD5 precursor, HSP 84, Ca2+ dependent phospholipase A2 precursor, and the ribosomal proteins, S12, S11, L12, L11, S29, S19, L21, L19, L13, L44, and L36.

37. A method of Claim 34 wherein the upregulated protein is selected from the group consisting of clusterin, T-cell surface glycoprotein CD5 precursor, HSP 84, and Ca2+ dependent phospholipase A2 precursor and the mRNA is for a protein selected from said group.

38. A method of Claim 1 wherein the protein is selected from the group consisting of cyclin D1, PLC-L, GRB2, ERK3/MAPK6, ERK1, ERK3, JNK2, CD40, CRAF1, C-MYC, PT-α, IL-R , CD40, C-MYC, PKC-α, GSTA1, GATA-2, PLGF, ezrin, HGF activator, hepatocyte growth factor-like protein, NCAD, MNDA, LHX1, TIE-1, NCAML1, CD104, CD44, SRC1, NMDA, TKT, ephrin (type A), Sp1, RAB proteins, PKC, TIR, Jak3, EGR-1, TNK1, CAMK IV, HSP40, HSP70, HSP60, HSO27,fMLP-related receptor, HSP27, glutaredoxin, CREB, gadd153, XPG, XPD, ubiqitin- conjugating enzyme, RAD23, cadherin 2, neural cell adhesion molecule, integrin alpha 3, leukocyte adhesion glycoprotein p150, integrin beta 4, TIE, NCAML1, α3β1 integrin, CD11C antigen, CD104 antigen, CD44, NMDA, TKT, ephrin (type A), and Sp1, a RAB protein, PKC, TfR, bcl-x and caspase-9.

39. A method of Claim 34 wherein the upregulated protein is selected from the group consisting of cyclin D1, PLC-L, GRB2, ERK3/MAPK6, ERK1, ERK3, JNK2, CD40, CRAF1, C-MYC, PT-α, IL-R, CD40, C-MYC, PKC-α, GSTA1, GATA-2, PLGF, ezrin, HGF activator, hepatocyte growth factor-like protein, NCAD, MNDA, LHX1, TIE-1, NCAML1, CD104, CD44, SRC1, NMDA, TKT, ephrin (type A), Sp1, RAB proteins, PKC, TIR, Jak3, EGR-1, TNK1, CAMK IV, HSP40, HSP70, HSP60, HSO27, fMLP-related receptor, HSP27, glutaredoxin, CREB, gadd153, XPG, XPD, ubiqitin- conjugating enzyme, RAD23, cadherin 2, neural cell adhesion molecule, integrin alpha 3, leukocyte adhesion glycoprotein p150, integrin beta 4, TIE, NCAML1, α3β1 integrin, CD11C antigen, CD104 antigen, CD44, NMDA, TKT, ephrin (type A), and Sp1, a RAB protein, PKC, TfR, , bcl-x and caspase-9. and the mRNA is for a protein selected from said group.

40. A method of Claim 1 wherein the protein is selected from the group consisting of an IL-2 receptor, a gamma c chain of an IL-2 receptor, intereron - γ, and a C-C chemokine.

41. A method of Claim 34 wherein the upregulated protein is selected from the group consisting of an IL-2 receptor, a gamma c chain of an IL-2 receptor, intereron - γ, and a C-C chemokine and the mRNA is for a protein selected from said group.

42. A method of Claim 1 wherein the protein is selected from the group consisting of cyclin D1, PLC-L, GRB2, ERK3/MAPK6, ERK1, ERK3, PKC-α, GSTA1, GATA-2, and PLGF.

43. A method of Claim 34 wherein the upregulated protein is selected from the group consisting of cyclin D1, PLC-L, GRB2, ERK3/MAPK6, ERK1, ERK3, JNK2, CD40, CRAF1, C-MYC, PT-α, IL-R, PKC-α, GSTA1, GATA-2, and PLGF and the mRNA is for a protein selected from said group.

44. A method of Claim 1 wherein the protein is selected from the group consisting of a RAB protein, PKC, and TfR.

45. A method of Claim 34 wherein the upregulated protein is selected from the group consisting of a RAB protein, PKC, and TfR and the mRNA is for a protein selected from said group.

46. A method of Claim 1 wherein the protein is selected from the group consisting of Jak 3, EGR-1, TNK1, and CAMK IV.

47. A method of Claim 34 wherein the upregulated protein is selected from the group consisting of Jak 3, EGR-1, TNK1, and CAMK IV and the mRNA is for a protein selected from said group.

48. A method of Claim 1 wherein the protein is selected from the group consisting of HSP40, HSP70, HSP60, HSO27, fMLP-related receptor, HSP27, glutaredoxin, CREB, gadd 153, XPG, XPD, ubiquitin, conjugating enzyme, RAD 23, and ataxia telengiectasia.

49. A method of Claim 34 wherein the upregulated protein is selected from the group consisting of HSP40, HSP70, HSP60, HSO27, fMLP-related receptor, HSP27, glutaredoxin, CREB, gadd 153, XPG, XPD, ubiquitin, conjugating enzyme, RAD 23, and ataxia telengiectasia and the mRNA is for a protein selected from said group.

50. A method of decreasing the levels of a protein in a Peyer's patch cell, said method comprising delivering to said cell a DNA molecule coding for an anti-sense nucleic acid molecule, a ribozyme nucleic acid molecule, an RNA interference nucleic acid molecule (RNAi), said anti-sense molecule, ribozyme or RNAi nucleic acid being complementary to a sequence of at least 10 nucleotides of the mRNA for said protein, wherein absent said anti-sense molecule, ribozyme or RNAi nucleic acid, the levels of said protein or its mRNA is less than in a non-Peyer's patch cell.

51. A method of increasing the extent to which the function of a protein is carried out in a Peyer's patch cell, said method comprising delivering to said cell a nucleic

acid coding for said protein, wherein absent said delivery, the level of said protein or its mRNA is greater in said cell than in a non-Peyer's patch cell.

52. A chimeric protein that comprises two or more segments, each of said segments enhancing a different step in the peptide transport process, said steps selected from the group consisting of binding to a cell, transporting the peptide into the cell, transporting the peptide through the cell, and transporting the peptide out of the cell.

53. A chimeric protein of Claim 52 wherein one of the segments binds to the cell.

54. A chimeric protein of Claim 52 wherein one of the segments is a protein that is more prevalent in a Peyer's patch cell than in a non-Peyer's patch cell.

55. A chimeric protein of Claim 52 wherein the cell is a Peyer's patch cell.

56. A chimeric protein of Claim 55 wherein the cell is an M cell.

57. A method of targeting a composition or delivery vehicle to a Peyer's patch cell said method comprising utilizing a composition or vehicle that contains a protein ligand that will specifically bind to a protein that is up-regulated in Peyer's patch cells.

58. The method of Claim 57 wherein the composition or delivery vehicle comprises a drug or antigen.

59. A method of selecting for a ligand that will selectively bind to a target in a Peyer's patch cell, said method comprising contacting a phage library with a protein that is upregulated in Peyer's patch cells.

60. The method of Claim 59 wherein the protein is attached to a solid substrate.

61. A method of Claim 1 wherein the protein is selected from the group consisting of HGF activator, ezrin, NCAD, MNDA, and LHX1.

62. A method of Claim 34 wherein the upregulated protein is selected from the group consisting of HGF activator, ezrin, NCAD, MNDA, and LHX1, and the mRNA is for a protein selected from said group.

63. A method of Claim 1 wherein the protein is selected from the group consisting of cadherin 2, neural cell adhesion molecule, integrin alpha 3, leukocyte adhesion glycoprotein p150, integrin beta 4, TIE, NCAML1, $\alpha 3\beta 1$ integrin, CD11C antigen, CD104 antigen, CD44, NMDA, TKT, ephrin (type A), and Sp1.

64. A method of Claim 34 wherein the upregulated protein is selected from the group consisting of cadherin 2, neural cell adhesion molecule, integrin alpha 3, leukocyte adhesion glycoprotein p150, integrin beta 4, TIE, NCAML1, $\alpha 3\beta 1$ integrin, CD11C antigen, CD104 antigen, CD44, NMDA, TKT, ephrin (type A), and Sp1, and the mRNA is for a protein

selected from said group.

65. A method of promoting enterocyte-M cell conversion, said method comprising orally administering an antigen, antigenic composition, or antigen-carrying particle to a person and either simultaneously with, or prior to, said administration, also orally administering a bacteria, or pro-biotic yogurts, or bacterial component to said person.

AMINO ACID SEQUENCES AND NUCLEOTIDE SEQUENCES CORRESPONDING TO SELECTED GENBANK ID NUMBERS

GENBANK ID: M81750
VERSION M81750.1 GI:895928

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GENBANK ID: X59798
VERSION X59798.1 GI:35631

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GENBANK ID: L27211.1
VERSION L27211.1 GI:558656

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GENBANK ID: U22398
VERSION U22398.1 GI:790247

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GENBANK ID: X51521
VERSION X51521.1 GI:31282

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GENBANK ID: L04143.1
VERSION L04143.1 GI:180574

THIS ENTRY IS NOT CONTIGUOUS GENOMIC DNA. IT CONTAINS NUMEROUS PIECES OF INTRONS.

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GENBANK ID:  M32110
VERSION     M32110.1  GI:189421

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GenBank ID: J04111
VERSION J04111.1 GI:186624

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GENBANK ID: X59932
VERSION X59932.1 GI:30255

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GENBANK ID: L29220
VERSION L29220.1 GI:632969

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GENBANK ID: M91815.1
VERSION M91815.1 GI:180169
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GENBANK ID: M26708
VERSION M26708.1 GI:190695

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GENBANK ID: M81757
VERSION M81757.1 GI:337732

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GENBANK ID: V00568
DEFINITION HUMAN MRNA ENCODING THE C-MYC ONCOGENE.
VERSION V00568.1 GI:34815

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GENBANK ID: L29219.1
VERSION L29219.1 GI:632963

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GENBANK ID: U49399.1
VERSION U49399.1 GI:1418220

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GENBANK ID: XM_039993.2
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4321 AGTACTGCCC CCCATGAGGA AGGAACAGCA ATGGTGTCAG TATCCAGGCT TTGTACAGAG
4381 TGCTTTTCTG TTTAGTTTTT ACTTTTTTTG TTTTGTTTTT TTAAAGACGA AATAAAGACC
4441 CAGGGGAGAA TGGGTGTTGT ATGGGGAGGC AAGTGTGGGG GGTCCTTCTC CACACCCACT
4501 TTGTCCATTT GCAAATATAT TTTGGAAAAC
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GENBANK ID: X14798.1

SEQUENCE 1:

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SYGIEHAQCVPPSEFSEPSFITESYQTLHPISSEELLSLKYENDYPSVILRDPLQTDT
LQNDYFAIKQEVVTPDNMCMGRTSRGKLGGQDSFESIESYDSCDRLTQSWSSQSSFNS
LQRVPSYDSFDSEDYPAALPNHKPKGTFKDYVRDRADLNKDKPVIPAAALAGYTGSGP
IQLWQFLLELLTDKSCQSFISWTGDGWEFKLSDPDEVARRWGKRKNKPKMNYEKLSRG
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SEQUENCE 2;

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SYGIEHAQCVPPSEFSEPSFITESYQTLHPISSEELLSLKYENDYPSVILRDPLQTDT
LQNDYFAIKQEVVTPDNMCMGRTSRGSGPIQLWQFLLELLTDKSCQSFISWTGDGWEF
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LGYTPEELHAMLDVKPDADE

GENBANK ID: D49547
VERSION D49547.1 GI:710654

MGKDYYQTLGLARGASDEEIKRAYRRQALRYHPDKNKEPGAEEK
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AEFFGGRNPFDTFFGQRNGEEGMDIDDPFSGFPMGMGGFTNVNFGRSRSAQEPARKKQ
DPPVTHDLRVSLEEIYSGCTKKMKISHKRLNPDGKSIRNEDKILTIEVKKGWKEGTKI
TFPKEGDQTSNNIPADIVFVLKDKPHNIFKRDGSDVIYPARISLREALCGCTVNVPTL
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EQVLPI

GENBANK ID: M11717
VERSION D49547.1 GI:710654

MGKDYYQTLGLARGASDEEIKRAYRRQALRYHPDKNKEPGAEEK
FKEIAEAYDVLSDPRKREIFDRYGEEGLKGSGPSGGSGGGANGTSFSYTFHGDPHAMF
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DPPVTHDLRVSLEEIYSGCTKKMKISHKRLNPDGKSIRNEDKILTIEVKKGWKEGTKI
TFPKEGDQTSNNIPADIVFVLKDKPHNIFKRDGSDVIYPARISLREALCGCTVNVPTL
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EQVLPI

GENBANK ID: X76648
VERSION X76648.1 GI:531404

MAQEFVNCKIQPGKVVVFIKPTCPYCRRAQEILSQLPIKQGLLE
FVDITATNHTNEIQDYLQQLTGARTVPRVFIGKDCIGGCSDLVSLQQSGELLTRLKQI
GALQ

GENBANK ID: NM_011587.1
VERSION NM_011587.1 GI:6755784

MVWWGSSLLLPTLFLASHVGASVDLTLLANLRITDPQRFFLTCV
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GPGCVKDCPGCLHGGVCHDHDGECVCPPGFTGTRCEQACREGRFGQSCQEQCPGTAGC
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SGWHGVHCEKSDRIPQILSMATEVEFNIGTMPRINCAAAGNPFPVRGSMKLRKPDGTM
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PRLLAKQSRQLVVSPLVSFSGDGPISSVRLHYRPQDSTIAWSAIVVDPSENVTLMNLK
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GPASPPAHVHLPPSGPPAPRHLHAQALSDSEIQLMWQHPEAPSGPISKYIVEIQVAGG
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DPVRESRAAEEGLDQQLVLAVVGSVSATCLTILAALLALVCIRRSCLHRRRTFTYQSG
SGEETILQFSSGTLTLTRRPKPQPEPLSYPVLEWEDITFEDLIGEGNFGQVIRAMIKK
DGLKMNAAIKMLKEYASENDHRDFAGELEVLCKLGHHPNIINLLGACENRGYLYIAIE
YAPYGNLLDFLRKSRVLETDPAFAREHGTASTLSSRQLLRFASDAANGMQYLSEKQFI
HRDLAARNVLVGENLASKIADFGLSRGEEVYVKKTMGRLPVRWMAIESLNYSVYTTKS
DVWSFGVLLWEIVSLGGTPYCGMTCAELYEKLPQGYRMEQPRNCDDEVYELMRQCWRD
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GENBANK ID: NM_002867.1
VERSION NM_002867.1 GI:4506368

MASVTDGKHGVKDASDQNFDYMFKLLIIGNSSVGKTSFLLRYAD
DTFTPAFVSTVGIDFKVKTVYRHEKRVKLQIWDTAGQERYRTITTAYYRGAMGFILMY
DITNEESFNAVQDWATQIKTYSWDNAQVILVGNKCDMEEERVVPTEKGQLLAEQLGFD
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GENBANK ID: P27361
NO VERSION DATA

LNENQKLAVKRILSGDCRPLPYILFGPPGTGKTVTIIEAVLQVH
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LIPLGLMSDISGQIVLAGDPMQLGPVIKSRLAMAYGLNVSFLERLMSRPAYQRDENAF
GACGAHNPLLVTKLVKNYRSHEALLMLPSRLFYHRELEVCADPTVVTSLLGWEKLPKK
GFPLIFHGVRGSEAREGKSPSWFNPAEAVQVLRYCCLLAHSISSQVSASDIGVITPYR
KQVEKIRILLRNVDLMDIKVGSVEEFQGQEYLVIIISTVRSNEDRFEDDRYFLGFLSN
SKRFNVAITRPKALLIVLGNPHVLVRDPCFGALLEYSITNGVYMGCDLPPALQSLQNC
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GENBANK ID: NM_002752.1
VERSION NM_002752.1 GI:4506096

MSDSKCDSQFYSVQVADSTFTVLKRYQQLKPIGSGAQGIVCAAF
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DVYLVMELMDANLCQVIHMELDHERMSYLLYQMLCGIKHLHSAGIIHRDLKPSNIVVK
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VKGCVIFQGTDHIDQWNKVIEQLGTPSAEFMKKLQPTVRNYVENRPKYPGIKFEELFP
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GENBANK ID: M22382.1
VERSION M22382.1 GI:190126

MLRLPTVFRQMRPVSRVLAPHLTRAYAKDVKFGADARALMLQGV
DLLADAVAVTMGPKGRTVIIEQSWGSPKVTKDGVTVAKSIDLKDKYKNIGAKLVQDVA
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PVTTPEEIAQVATISANGDKEIGNIISDAMKKVGRKGVITVKDGKTLNDELEIIEGMK
FDRGYISPYFINTSKGQKCEFQDAYVLLSEKKISSIQSIVPALEIANAHRKPLVIIAE
DVDGEALSTLVLNRLKVGLQVVAVKAPGFGDNRKNQLKDMAIATGGAVFGEEGLTLNL
EDVQPHDLGKVGEVIVTKDDAMLLKGKGDKAQIEKRIQEIIEQLDVTTSEYEKEKLNE
RLAKLSDGVAVLKVGGTSDVEVNEKKDRVTDALNATRAAVEEGIVLGGGCALLRCIPA
LDSLTPANEDQKIGIEIIKRTLKIPAMTIAKNAGVEGSLIVEKIMQSSSEVGYDAMAG
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GENBANK ID: U09564.1
DEFINITION HUMAN SERINE KINASE MRNA, COMPLETE CDS.
VERSION U09564.1 GI:507212

MERKVLALQARKKRTKAKKDKAQRKSETQHRGSAPHSESDLPEQ
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ICMVFEVLGHHLLKWIIKSNYQGLPLPCVKKIIQQVLQGLDYLHTKCRIIHTDIKPEN
ILLSVNEQYIRRLAAEATEWQRSGAPPPSGSAVSTAPQPKPADKMSKNKKKKLKKKQK
RQAELLEKRMQEIEEMEKESGPGQKRPNKQEESESPVERPLKENPPNKMTQEKLEESS
TIGQDQTLMERDTEGGAAEINCNGVIEVINYTQNSNNETLRHKEDLHNANDCDVQNLN
QESSFLSLPNGDSSTSQETDSCTPITSEVSDTMVCQSSSTVGQSFSEQHISQLQESIR
AEIPCEDEQEQEHNGPLDNKGKSTAGNFLVNPLEPKNAEKLKVKIADLGNACWVHKHF
TEDIQTRQYRSLEVLIGSGYNTPADIWSTACMAFELATGDYLFEPHSGEEYTRDEDHI
ALIIELLGKVPRKLIVAGKYSKEFFTKKGDLKHITKLKPWGLFEVLVEKYEWSQEEAA
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GENBANK ID: M11507.1
VERSION M11507.1 GI:339515

MMDQARSAFSNLFGGEPLSYTRFSLARQVDGDNSHVEMKLAVDE
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KDENLALYVENQFREFKLSKVWRDQHFVKIQVKDSAQNSVIIVDKNGRLVYLVENPGG
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IGVLIYMDQTKFPIVNAELSFFGHAHLGTGDPYTPGFPSFNHTQFPPSRSSGLPNIPV
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ASWSAGDFGSVGATEWLEGYLSSLHLKAFTYINLDKAVLGTSNFKVSASPLLYTLIEK
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GTTMDTYKELIERIPELNKVARAAAEVAGQFVIKLTHDVELNLDYERYNSQLLSFVRD
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GENBANK ID: U55017.1
VERSION U55017.1 GI:1297296

MESYHKPDQQKLQALKDTANRLRISSIQATTAAGSGHPTSCCSA
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GSVWEAMAFASIYKLDNLVAILDINRLGQSDPAPLQHQMDIYQKRCEAFGWHAIIVDG
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GVTLHEALAAAELLKKEKINIRVLDPFTIKPLDRKLILDSARATKGRILTVEDHYYEG
GIGEAVSSAVVGEPGITVTHLAVNRVPRSGKPAELLKMFGIDRDAIAQAVRGLITKA

GENBANK ID: X14034.
VERSION X14034.1 GI:35513

MSTTVNVDSLAEYEKSQIKRALELGTVMTVFSFRKSTPERRTVQ
VIMETRQVAWSKTADKIEGFLDIMEIKEIRPGKNSKDFERAKAVRQKEDCCFTILYGT
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ISLRELKTILPLINFKVSSAKFLKDKFVEIGAHKDELSFEQFHLFYKKLMFEQQKSIL
DEFKKDSSVFILGNTDRPDASAVYLHDFQRFLIHEQQEHWAQDLNKVRERMTKFIDDT
MRETAEPFLFVDEFLTYLFSRENSIWDEKYDAVDMQDMNNPLSHYWISSSHNTYLTGD
QLRSESSPEAYIRCLRMGCRCIELDCWDGPDGKPVIYHGWTRTTKIKFDDVVQAIKDH
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IIIKHKKLGPRGDVDVNMEDKKDEHKQQGELYMWDSIDQKWTRHYCAIADAKLSFSDD
IEQTMEEEVPQDIPPTELHFGEKWFHKKVEKRTSAEKLLQEYCMETGGKDGTFLVRES
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VSKEPGGWWKGDYGTRIQQYFPSNYVEDISTADFEELEKQIIEDNPLGSLCRGILDLN
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ICGAEYGNNKFKTTVVNDNGLSPIWAPTQEKVTFEIYDPNLAFLRFVVYEEDMFSDPN
FLAHATYPIKAVKSGFRSVPLKNGYSEDIELASLLVFCEMRPVLESEEELYSSCRQLR
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GENBANK ID: M27691.1|
VERSION M27691.1 GI:181038

MTMESGAENQQSGDAAVTEAENQQMTVQAQPQIATLAQVSMPAA
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YQTSSGQYIAITQGGAIQLANNGTDGVQGLQTLTMTNAAATQPGTTILQYAQTTDGQQ
ILVPSNQVVVQAASGDVQTYQIRTAPTSTIAPGVVMASSPALPTQPAEEAARKREVRL
MKNREAARECRRKKKEYVKCLENRVAVLENQNKTLIEELKALKDLYCHKSD

GENBANK ID: M18391
VERSION M18391.1 GI:339716

MERRWPLGLGLVLLLCAPLPPGARAKEVTLMDTSKAQGELGWLL
DPPKDGWSEQQQILNGTPLYMYQDCPMQGRRDTDHWLRSNWIYRGEEASRVHVELQFT
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SGSVKLNVERCSLGRLTRRGLYLAFHNPGACVALVSVRVFYQRCPETLNGLAQFPDTL
PGPAGLVEVAGTCLPHARASPRPSGAPRMHCSPDGEWLVPVGRCHCEPGYEEGGSGEA
CVACPSGSYRMDMDTPHCLTCPQQSTAESEGATICTCESGHYRAPGEGPQVACTGPPS
APRNLSFSASGTQLSLRWEPPADTGGRQDVRYSVRCSQCQGTAQDGGPCQPCGVGVHF

SPGARALTTPAVHVNGLEPYANYTFNVEAQNGVSGLGSSGHASTSVSISMGHAESLSG
LSLRLVKKEPRQLELTWAGSRPRSPGANLTYELHVLNQDEERYQMVLEPRVLLTELQP
DTTYIVRVRMLTPLGPGPFSPDHEFRTSPPVSRGLTGGEIVAVIFGLLLGAALLLGIL
VFRSRRAQRQRQQRHVTAPPMWIERTSCAEALCGTSRHTRTLHREPWTLPGGWSNFPS
RELDPAWLMVDTVIGEGEFGEVYRGTLRLPSQDCKTVAIKTLKDTSPGGQWWNFLREA
TIMGQFSHPHILHLEGVVTKRKPIMIITEFMENAALDAFLREREDQLVPGQLVAMLQG
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VDCPAPLYELMKNCWAYDRARRPHFQKLQAHLEQLLANPHSLRTIANFDPRVTLRLPS
LSGSDGIPYRTVSEWLESIRMKRYILHFHSAGLDTMECVLELTAEDLTQMGITLPGHQ
KRILCSIQGFKD

GENBANK ID: X54079.1
VERSION X54079.1 GI:32477

MTERRVPFSLLRGPSWDPFRDWYPHSRLFDQAFGLPRLPEEWSQ
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GTLTVEAPMPKLATQSNEITIPVTFESRAQLGGPEAAKSDETAAK

GENBANK ID: XM_012654.3
VERSION XM_012654.3 GI:14773503

MFGVTLWEMFSGGEEPWAGVPPYLILQRLEDRARLPRPPLCSRA
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GENBANK ID: XM_054457.2
VERSION XM_054457.2 GI:18590931

MASATDSRYGQKESSDQNFDYMFKILIIGNSSVGKTSFLFRYAD
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AC

GENBANK ID: XM_038595.3
VERSION XM_038595.3 GI:18590923

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FGDHLAEDLCVQAAKASGILPVYHSLFALATEDLSCWFPPSHIFSVEDASTQVLLYRI
RFYFPNWFGLEKCHRFGLRKDLASAILDLPVLEHLFAQHRSDLVSGRLPVGLSLKEQG
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LPEALSFVALVDGYFRLTTDSQHFFCKEVAPPRLLEEVAEQCHGPITLDFAINKLKTG
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RELLATCWDGGLHVDGVAVTLTSCCIPRPKEKSNLIVVQRGHSPPTSSLVQPQSQYQL
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MLTDRIPWVAPECLREAQTLSLEADKWGFGATVWEVFSGVTMPISALDPAKKLQFYED
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RDGLWNGAQLYACQDPTIFEERHLKYISQLGKGNFGSVELCRYDPLGDNTGALVAVKQ
LQHSGPDQQRDFQREIQILKALHSDFIVKYRGVSYGPGRQSLRLVMEYLPSGCLRDFL
QRHRARLDASRLLLYSSQICKGMEYLGSRRCVHRDLAARNILVESEAHVKIADFGLAK
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SAEFLRMMGCERDVPALCRLLELLEEGQRLPAPPACPAEVHELMKLCWAPSPQDRPSF
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GENBANK ID: NM_002755.2
VERSION NM_002755.2 GI:14589898

MPKKKPTPIQLNPAPDGSAVNGTSSAETNLEALQKKLEELELDE
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IPEQILGKVSIAVIKGLTYLREKHKIMHRDVKPSNILVNSRGEIKLCDFGVSGQLIDS
MANSFVGTRSYMSPERLQGTHYSVQSDIWSMGLSLVEMAVGRYPIPPPDAKELELMFG
CQVEGDAAETPPRPRTPGRPLSSYGMDSRPPMAIFELLDYIVNEPPPKLPSGVFSLEF
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GENBANK ID: NM_001744.1
VERSION NM_001744.1 GI:4502556

MLKVTVPSCSASSCSSVTASAAPGTASLVPDYWIDGSNRDALSD
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VRKLIVLDPKKRLTTFQALQHPWVTGKAANFVHMDTAQKKLQEFNARRKLKAAVKAVV
ASSRLGSASSSHGSIQESHKASRDPSPIQDGNEDMKAIPEGEKIQGDGAQAAVKGAQA
ELMKVQALEKVKGADINAEEAPKMVPKAVEDGIKVADLELEEGLAEEKLKTVEEAAAP
REGQGSSAVGFEVPQQDVILPEY

GENBANK ID: XM_053461.2
VERSION XM_053461.2 GI:18553657

MASRGATRPNGPNTGNKICQFKLVLLGESAVGKSSLVLRFVKGQ
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GENBANK ID: U33635.1
VERSION U33635.1 GI:1016701

MGAARGSPARPRRLPLLSVLLLPLLGGTQTAIVFIKQPSSQDAL
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IADESFARVVLAPQDVVVARYEEAMFHCQFSAQPPPSLQWLFEDETPITNRSRPPHLR
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3241 TCTGGACCAG GAATTAGTTG CTGTGGGTGC CACAGCTGAA GTCAGTTTGT CTTGCTGGTT
3301 TAAATAGATC TTTCAGAGCT GGGTGCTGGG TTTGCCATCT TTTTGTTTTC TTTGAAAAGC
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3421 AA
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GENBANK ID: D26155.1
VERSION D26155.1 GI:505086

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GENBANK ID: M62829.1
VERSION M62829.1 GI:182262

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GENBANK ID: U10421.1
VERSION U10421.1 GI:500756

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GENBANK ID: U08015.1

VERSION U08015.1 GI:500631

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GENBANK ID: U08191.1
VERSION U08191.1 GI:476273

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GENBANK ID: M55654
VERSION M55654.1 GI:339491

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GENBANK ID: NM_005568.1
VERSION NM_005568.1 GI:5031866

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GENBANK ID: X69111.1
VERSION X69111.1 GI:32294

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GENBANK ID: NP_000507.1
VERSION NP_000507.1 GI:4504047

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 121 NPENQFRVDY ILSVMNVPDF DFPPEFYEHA KALWEDEGVR ACYERSNEYQ LIDCAQYFLD
 181 KIDVIKQADY VPSDQDLLRC RVLTSGIFET KFQVDKVNFH MFDVGGQRDE RRKWIQCFND
 241 VTAIIFVVAS SSYNMVIRED NQTNRLQEAL NLFKSIWNNR WLRTISVILF LNKQDLLAEK
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GENBANK ID: AAA40889.1
VERSION AAA40889.1 GI:203357

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 121 QVQGQQGQTQ QIIIQQPQTA VTAGQTQTQQ QIAVQGQQVA QTAEGQTIVY QPVNADGTIL
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GENBANK ID: B53771
VERSION B53771 GI:2136296

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 181 KRTSVFIQVH CISTEFTMRK HGGEKGVPFR VQIDTFKENE NGEYTEHLHS ASCQIKVFKP
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GENBANK ID: M92299.1
VERSION M92299.1 GI:184292

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GENBANK ID: M68891.1
VERSION M68891.1 GI:182995

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GENBANK ID: XM_028606.2
VERSION XM_028606.2 GI:15304625

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GENBANK ID: NP_009077.1
DEFINITION HOMO SAPIENS ZINC FINGER PROTEIN 161 (ZNF161), MRNA.
VERSION NM_007146.1 GI:6005967
CDS 42..1592
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421 CGTTGGTCTC GACCATTGCA GGCATCTTGT CAACAGTCAC TACATCTTCC TCGGGCACCA
481 ACCCCAGTAG CAGTGCCAGC ACCACAGCTA TGCCAGTGAC CCAGTCTGTC AAGAAACCCA
541 GTAAGCCTGT CAAGAAGAAC CATGCTTGTG AGATGTGTGG GAAGGCCTTC CGAGATGTGT
601 ACCATCTCAA TCGACACAAG CTCTCCCATT CAGATGAGAA ACCCTTTGAG TGTCCTATTT
661 GTAATCAGCG CTTCAAGAGG AAGGACCGGA TGACTTACCA TGTGAGGTCT CATGAAGGAG
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781 TAAGCTGTCA TGTAAAACAT GTCCATTCAA CAGAAAGACC CTTCAAATGC CAAACGTGCA
841 CTGCTGCCTT TGCCACCAAA GACAGACTGC GGACACACAT GGTGCGCCAT GAAGGCAAGG
901 TATCATGTAA CATCTGTGGG AAGCTCCTGA GTGCAGCATA CATCACCAGC CACTTAAAGA
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GENBANK ID: AAA36598.1
DEFINITION HUMAN STEM CELL PROTEIN (SCL) MRNA, COMPLETE CDS.
VERSION M29038.1 GI:337958
CDS 81..725
/CODON_START=1

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 241 CTTCCCCCTA TGAGATGGAG ATTACTGATG GTCCCCACAC CAAAGTTGTG CGGCGTATCT
 301 TCACCAACAG CCGGGAGCGA TGGCGGCAGC AGAATGTGAA CGGGGCCTTT GCCGAGCTCC
 361 GCAAGCTGAT CCCCACACAT CCCCCGGACA AGAAGCTCAG CAAGAATGAG ATCCTCCGCC
 421 TGGCCATGAA GTATATCAAC TTCTTGGCCA AGCTGCTCAA TGACCAGGAG GAGGAGGGCA
 481 CCCAGCGGGC CAAGACTGGC AAGGACCCTG TGGTGGGGGC TGGTGGGGGT GGAGGTGGGG
 541 GAGGGGGCGG CGCGCCCCCA GATGACCTCC TGCAAGACGT GCTTTCCCCC AACTCCAGCT
 601 GCGGCAGCTC CCTGGATGGG GCAGCCAGCC CGGACAGCTA CACGGAGGAG CCCGCGCCCA
 661 AGCACACGGC CCGCAGCCTC CATCCTGCCA TGCTGCCTGC CGCCGATGGA GCCGGCCCTC
 721 GGTGATGGGT CTGGGCCACC AGGATCAGCC AGGAGGGCGT TCTTAGGCTG CTGGGATGGT
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 961 GGCACGGTCT TCCCTCTTCC CTCAGTCCCA AATCCTTCCC AAGTAAGAGG CTGGAGTTGT
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GENBANK ID: M27492.1
VERSION M27492.1 GI:186289

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GENBANK ID: L34059
VERSION L34059.1 GI:506409

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GENBANK ID: M77640
VERSION M77640.1 GI:186053

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GENBANK ID: M59911.1
VERSION M59911.1 GI:186496

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GENBANK ID: M81695.1
VERSION M81695.1 GI:487829

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GENBANK ID: X51841.1
VERSION X51841.1 GI:33910

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GENBANK ID: XP_030326.1
VERSION XP_030326.1 GI:14763626

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181 GSSSERSSTS GGYIFYTFST VHPIPDEDSP WITDSTDRIP ATTLMSTSAT ATETATKRQE
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301 EDFISSTIST TPRAFDHTKQ NQDWTQWNPS HSNPEVLLQT TTRMTDVDRN GTTAYEGNWN
361 PEAHPPLIHH EHHEEEETPH STSTIQATPS STTEETATQK EQWFGNRWHE GYRQTPKEDS
421 HSTTGTAAAS AHTSHPMQGR TTPSPEDSSW TDFFNPISHP MGRGHQAGRR MDMDSSHSIT
481 LQPTANPNTG LVEDLDRTGP LSMTTQQSNS QSFSTSHEGL EEDKDHPTTS TLTSSNRNDV
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601 SLSGDQDTFH PSGGSHTTHG SESDGHSHGS QEGGANTTSG PIRTPQIPEW LIILASLLAL
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GENBANK ID: NP_000826.1
VERSION NP_000826.1 GI:4504129

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61 EIQPLTVGVN TTNPSSLLTQ ICGLLGAAHV HGIVFEDNVD TEAVAQILDF ISSQTHVPIL
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361 IALNRHRLWE MVGRWEHGVL YMKYPVWPRY SASLQPVVDS RHLTVATLEE RPFVIVESPD
421 PGTGGCVPNT VPCRRQSNHT FSSGDVAPYT KLCCKGFCID ILKKLARVVK FSYDLYLVTN
481 GKHGKRVRGV WNGMIGEVYY KRADMAIGSL TINEERSEIV DFSVPFVETG ISVMVARSNG
541 TVSPSAFLEP YSPAVWVMMF VMCLTVVAIT VFMFEYFSPV SYNQNLTRGK KSGGPAFTIG
601 KSVWLLWALV FNNSVPIENP RGTTSKIMVL VWAFFAVIFL ASYTANLAAF MIQEQYIDTV
661 SGLSDKKFQR PQDQYPPFRF GTVPNGSTER NIRSNYRDMH THMVKFNQRS VEDALTSLKM
721 GKLDAFIYDA AVLNYMAGKD EGCKLVTIGS GKVFATTGYG IAMQKDSHWK RAIDLALLQF
781 LGDGETQKLE TVWLSGICQN EKNEVMSSKL DIDNMAGVFY MLLVAMGLAL LVFAWEHLVY
841 WKLRHSVPNS SQLDFLLAFS RGIYSCFSGV QSLASPPRQA SPDLTASSAQ ASVLKMLQAA
901 RDMVTTAGVS SSLDRATRTI ENWGGGRRAP PPSPCPTPRS GPSPCLPTPD PPPEPSPTGW
961 GPPDGGRAAL VRRAPQPPGR PPTPGPPLSD VSRVSRRPAW EARWPVRTGH CGRHLSASER

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1021 PLSPARCHYS SFPRADRSGR PFLPLFPEPP ELEDLPLLGP EQLARREALL HAAWARGSRP
1081 RHASLPSSVA EAFARPSSLP AGCTGPACAR PDGHSACRRL AQAQSMCLPI YREACQEGEQ
1141 AGAPAWQHRQ HVCLHAHAHL PFCWGAVCPH LPPCASHGSW LSGAWGPLGH RGRTLGLGTG
1201 YRDSGGLDEI SSVARGTQGF PGPCTWRRIS SLESEV
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GENBANK ID:  CAA43045.1

DEFINITION  HUMAN CDW40 MRNA FOR NERVE GROWTH FACTOR RECEPTOR-RELATED
            B-LYMPHOCYTE ACTIVATION MOLECULE.
VERSION     X60592.1  GI:29850
CDS             48..881
/CODON_START=1

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 121 CATGCAGAGA AAAACAGTAC CTAATAAACA GTCAGTGCTG TTCTTTGTGC CAGCCAGGAC
 181 AGAAACTGGT GAGTGACTGC ACAGAGTTCA CTGAAACGGA ATGCCTTCCT TGCGGTGAAA
 241 GCGAATTCCT AGACACCTGG AACAGAGAGA CACACTGCCA CCAGCACAAA TACTGCGACC
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 421 GCTCGCCCGG CTTTGGGGTC AAGCAGATTG CTACAGGGGT TTCTGATACC ATCTGCGAGC
 481 CCTGCCCAGT CGGCTTCTTC TCCAATGTGT CATCTGCTTT CGAAAAATGT CACCCTTGGA
 541 CAAGCTGTGA GACCAAAGAC CTGGTTGTGC AACAGGCAGG CACAAACAAG ACTGATGTTG
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 781 CCAACACTGC TGCTCCAGTG CAGGAGACTT TACATGGATG CCAACCGGTC ACCCAGGAGG
 841 ATGGCAAAGA GAGTCGCATC TCAGTGCAGG AGAGACAGTG AGGCTGCACC CACCCAGGAG
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GENBANK ID:  AAB59544.1
DEFINITION  HUMAN NERVE GROWTH FACTOR RECEPTOR MRNA, COMPLETE CDS.
VERSION     M14764.1  GI:189204
CDS             114..1397
/CODON_START=1

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 181 TGTCCCTTGG AGGTGCCAAG GAGGCATGCC CCACAGGCCT GTACACACAC AGCGGTGAGT
 241 GCTGCAAAGC CTGCAACCTG GGCGAGGGTG TGGCCCAGCC TTGTGGAGCC AACCAGACCG
 301 TGTGTGAGCC CTGCCTGGAC AGCGTGACGT TCTCCGACGT GGTGAGCGCG ACCGAGCCGT
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 961 AAGGAGCCAA CAGCCGGCCA GTGAACCAGA CGCCCCCACC AGAGGGAGAA AAACTCCACA
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2401 GTCAGGGACC AAGGACCCCT CACCTTGCAA CACACAGACA CACGCACACA CACACACAGG
2461 AGGAGAAATC TCACTTTTCT CCATGAGTTT TTTCTCTTGG GCTGAGACTG GATACTGCCC
2521 GGGGCAGCTG CCAGAGAAGC ATCGGAGGGA ATTGAGGTCT GCTCGGCCGT CTTCACTCGC
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3061 TGAGGGGAGG AAACTCACCT GCTGGCCCCT CACCTGGGCA CCTGGGGAGT GGGACAGAGT
3121 CTGGGTGTAT TTATTTTCCT CCCCAGCAGG TGGGGAGGGG GTTTGGTGGC TTGCAAGTAT
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3361 TAAGTGATGA ACATTAAATA GCAAAG
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GENBANK ID: NP_002502.1
VERSION NM_002511.1 GI:4505406
CDS 140..1312
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 241 CGGGACCACC ACGGAGTTGG TGATCCGCTG TGTGATCCCG TCCCTCTACC TGCTCATCAT
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 361 GAGGAGCGTC CCCAACATCT TCATCTCTAA CCTGGCGGCC GGGGACTTGC TGCTGCTGCT
 421 CACCTGCGTC CCGGTGGACG CCTCGCGCTA CTTCTTCGAC GAGTGGATGT TTGGCAAGGT
 481 GGGCTGCAAA CTGATCCCTG TCATCCAGCT CACTTCCGTG GGGGTTTCCG TGTTCACTCT
 541 CACTGCCCTC AGCGCCGACA GGTACAGAGC CATCGTTAAC CCCATGGACA TGCAGACGTC
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1021 TGAGATTGAT CCATCTCTAG GCCACATGAT TGTCACCTTA GTTGCCCGGG TTCTCAGTTT
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1201 ACTCAGCTCT TCAGCGGTGC GTATGACATC TCTGAAAAGC AATGCTAAGA ACATGGTGAC
1261 CAATTCTGTT TTACTAAATG GGCACAGCAT GAAGCAGGAA ATGGCAATGT GATTTTGGCC
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GENBANK ID: Q00941
EST
DNA TYPE: CDNA

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GENBANK ID: P05106
EST
DNA TYPE: CDNA
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EST GENBANK ACC: BF115658
DNA TYPE: CDNA

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EST
GENBANK ACC: BF062996
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GENBANK ID: CAA52348.1
VERSION X74295.1 GI:437781
CDS <1..234
/CODON_START=1

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61 GTGAAGATTC CTCGGGAAGA CCGACAGCAG TTCAAGGAGG AGAAGACGGG CACCATCCTG

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       121 AGGAACAACT GGGGCAGCCC CCGGCGGGAG GGCCCGGATG CACACCCCAT CCTGGCTGCT
       181 GACGGGCATC CCGAGCTGGG CCCCGATGGG CATCCAGGGC CAGGCACCGC CTAGGTTCCC
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       421 GTGAGATGAG AGTGGGTAAA TCAGGGACAG GGCCATGGGG TAGGGTGAGA AGGGCAGGGG
       481 TGTCCTGATG CAAAGGTGGG GAGAAGGATC CTAATCCCTT CCTCTCCCAT TCACCCTGTG
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       601 GGTTGTGTCA CTGACTCAAG GCTGCTCCTT CTCTAGTTTC CCCTCTCATC TGACCTTAGT
       661 TTGCTGCCAT CAGTCTAGTG GTTTCGTGGT TTCGTCTATT TATTAAAAAA TCGGAACCC
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GENBANK ID: M57627
VERSION CAA51942.1 GI:580177
1 MHSSAL

GENBANK ID: AAA52578.1
VERSION AAA52578.1 GI:183364

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        61 SEMFDLQEPT CLQTRLELYK QGLRGSLTKL KGPLTMMASH YKQHCPPTPE TSCATQIITF
       121 ESFKENLKDF LLVIPFDCWE PVQE
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GENBANK ID: AAA58482.1
VERSION AAA58482.1 GI:182669

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         1 METNFSIPLN ETEEVLPEPA GHTVLWIFSL LVHGVTFVFG VLGNGLVIWV AGFRMTRTVN
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       121 LDRCICVLHP AWAQNHRTMS LAKRVMTGLW IFTIVLTLPN FIFWTTISTT NGDTYCIFNF
       181 AFWGDTAVER LNVFITMAKV FLILHFIIGF TVPMSIITVC YGIIAAKIHR NHMIKSSRPL
       241 RVFAAVVASF FICWFPYELI GILMAVWLKE MLLNGKYKII LVLINPTSSL AFFNSCLNPI
       301 LYVFMGRNFQ ERLIRSLPTS LERALTEVPD SAQTSNTHTT SASPPEETEL QAM
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GENBANK ID: P17774
VERSION P17774 GI:121324

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         1 MSESLVVCDV AEDLVEKLRK FRFRKETNNA AIIMKIDKDK RLVVLDEELE GISPDELKDE
        61 LPERQPRFIV YSYKYQHDDG RVSYPLCFIF SSPVGCKPEQ QMMYAGSKNK LVQTAELTKV
       121 FEIRNTEDLT EEWLREKLGF FH
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GENBANK ID: P51858
VERSION P51858 GI:1708157

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         1 MSRSNRQKEY KCGDLVFAKM KGYPHWPARI DEMPEAAVKS TANKYQVFFF GTHETAFLGP
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       181 EAATLEVERP LPMEVEKNST PSEPGSGRGP PQEEEEEEDE EEEATKEDAE APGIRDHESL
       241
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GENBANK ID: P10147
VERSION P10147 GI:127078

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        61 GVIFLTKRSR QVCADPSEEW VQKYVSDLEL SA
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GENBANK ID: P13500
VERSION P13500 GI:126842

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         1 MKVSAALLCL LLIAATFIPQ GLAQPDAINA PVTCCYNFTN RKISVQRLAS YRRITSSKCP
        61 KEAVIFKTIV AKEICADPKQ KWVQDSMDHL DKQTQTPKT
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GENBANK ID: NP_065391.1
VERSION NP_065391.1 GI:10092621

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       61 RIQGLDVPKL REHCRERPGA FPSEETLRGL GRRGFLQTLN ATLGCVLHRL ADLEQRLPKA
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      181 ASDAFQRKLE GCRFLHGYHR FMHSVGRVFS KWGESPNRSR RHSPHQALRK GVRRTRPSRK
      241 GKRLMTRGQL PR

GENBANK ID:  XP_013053.3
VERSION     XP_013053.3  GI:14768277

        1 MEKERETLQA WKERVGQELD RVVAFWMEHS HDQEHGGFFT CLGREGRVYD DLKYVWLQGR
       61 QVWMYCRLYR TFERFRHAQL LDAAKAGGEF LLRYARVAPP GKKCAFVLTR DGRPVKVQRT
      121 IFSECFYTMA MNELWRATGE VRYQTEAVEM MDQIVHWVQE DASGLGRPQL QGAPAAEPMA
      181 VPMMLLNLVE QLGEADEELA GKYAELGDWC ARRILQHVQR DGQAVLENVS EGGKELPGCL
      241 GRQQNPGHTL EAGWFLLRHC IRKGDPELRA HVIDKFLLLP FHSGWDPDHG GLFYFQDADN
      301 FCPTQLEWAM KLWWPHSEAM IAFLMGYSDS GDPVLLRLFY QVAEYTFRQF RDPEYGEWFG
      361 YLSREGKVAL SIKGGPFKGC FHVPRCLAMC EEMLGALLSR PAPAPSPAPT PACRGAE

GENBANK ID:  B31848
VERSION     B31848  GI:87005

        1 MTCKMSQLER NIETIINTFH QYSVKLGHPD TLNQGEFKEL VRKDLQNFLK KENKNEKVIE
       61 HIMEDLDTNA DKQLSFEEFI MLMARLTWAS HEKMHEGDEG PGHHHKPGLG EGTP

GENBANK ID:  CAA38698.1
VERSION     CAA38698.1  GI:35522

        1 MPVMRLFPCF LQLLAGLALP AVPPQQWALS AGNGSSEVEV VPFQEVWGRS YCRALERLVD
       61 VVSEYPSEVE HMFSPSCVSL LRCTGCCGDE NLHCVPVETA NVTMQLLKIR SGDRPSYVEL
      121 TFSQHVRCEC RPLREKMKPE RCGDAVPRR

GENBANK ID:  AAA35789.1
VERSION     AAA35789.1  GI:181971

        1 MNFLLSWVHW SLALLLYLHH AKWSQAAPMA EGGGQNHHEV VKFMDVYQRS YCHPIETLVD
       61 IFQEYPDEIE YIFKPSCVPL MRCGGCCNDE GLECVPTEES NITMQIMRIK PHQGQHIGEM
      121 SFLQHNKCEC RPKKDRARQE NPCGPCSERR KHLFVQDPQT CKCSCKNTDS RCKARQLELN
      181 ERTCRCDKPR R

GENBANK ID:  AAA66062.1
VERSION     AAA66062.1  GI:536898

        1 MWKRWLALAL ALVAVAWVRA EEELRSKSKI CANVFCGAGR ECAVTEKGEP TCLCIEQCKP
       61 HKRPVCGSNG KTYLNHCELH RDACLTGSKI QVDYDGHCKE KKSVSPSASP VVCYQSNRDE
      121 LRRRIIQWLE AEIIPDGWFS KGSNYSEILD KYFKNFDNGD SRLDSSEFLK FVEQNETAIN
      181 ITTYPDQENN KLLRGLCVDA LIELSDENAD WKLSFQEFLK CLNPSFNPPE KKCALEDETY
      241 ADGAETEVDC NRCVCACGNW VCTAMTCDGK NQKGAQTQTE EEMTRYVQEL QKHQETAEKT
      301 KRVSTKEI

GENBANK ID:  AAA59872.1
VERSION     AAA59872.1  GI:398038

        1 MGWLPLLLLL TQCLGVPGQR SPLNDFQVLR GTELQHLLHA VVPGPWQEDV ADAEECAGRC
       61 GPLMDCRAFH YNVSSHGCQL LPWTQHSPHT RLRRSGRCDL FQKKDYVRTC IMNNGVGYRG
      121 TMATTVGGLP CQAWSHKFPN DHKYTPTLRN GLEENFCRNP DGDPGGPWCY TTDPAVRFQS
      181 CGIKSCREAA CVWCNGEEYR GAVDRTESGR ECQRWDLQHP HQHPFEPGKF LDQGLDDNYC
      241 RNPDGSERPW CYTTDPQIER EFCDLPRCGS EAQPRQEATT VSCFRGKGEG YRGTANTTTA
      301 GVPCQRWDAQ IPHQHRFTPE KYACKDLREN FCRNPDGSEA PWCFTLRPGM RAAFCYQIRR
      361 CTDDVRPQDC YHGAGEQYRG TVSKTRKGVQ CQRWSAETPH KPQFTFTSEP HAQLEENFCR
      421 NPDGDSHGPW CYTMDPRTPF DYCALRRCAD DQPPSILDPP DQVQFEKCGK RVDRLDQRRS
      481 KLRVVGGHPG NSPWTVSLRN RQGQHFCGGS LVKEQWILTA RQCFSSCHMP LTGYEVWLGT
      541 LFQNPQHGEP SLQRVPVAKM VCGPSGSQLV LLKLERSVTL NQRVALICLP PEWYVVPPGT
      601 KCEIAGWGET KGTGNDTVLN VAFLNVISNQ ECNIKHRGRV RESEMCTEGL LAPVGACEGD
      661 YGGPLACFTH NCWVLEGIII PNRVCARSRW PAVFTRVSVF VDWIHKVMRL G

GENBANK ID:  P01579
VERSION     P01579  GI:124479
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     61 EESDRKIMQS QIVSFYFKLF KNFKDDQSIQ KSVETIKEDM NVKFFNSNKK KRDDFEKLTN
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GENBANK ID: XP_035842.1
DEFINITION HOMO SAPIENS SMALL INDUCIBLE CYTOKINE A5 (RANTES) (SCYA5), MRNA.

CDS 22..297
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    241 GCCAACCCAG AGAAGAAATG GGTTCGGGAG TACATCAACT CTTTGGAGAT GAGCTAGGAT
    301 GGAGAGTCCT TGAACCTGAA CTTACACAAA TTTGCCTGTT TCTGCTTGCT CTTGTCCTAG
    361 CTTGGGAGGC TTCCCCTCAC TATCCTACCC CACCCGCTCC TTGAAGGGCC CAGATTCTAC
    421 CACACAGCAG CAGTTACAAA AACCTTCCCC AGGCTGGACG TGGTGGCTCA CGCCTGTAAT
    481 CCCAGCACTT TGGGAGGCCA AGGTGGGTGG ATCACTTGAG GTCAGGAGTT CGAGACCAGC
    541 CTGGCCAACA TGATGAAACC CCATCTCTAC TAAAAATACA AAAAATTAGC CGGGCGTGGT
    601 AGCGGGCGCC TGTAGTCCCA GCTACTCGGG AGGCTGAGGC AGGAGAATGG CGTGAACCCG
    661 GGAGGCGGAG CTTGCAGTGA GCCGAGATCG CGCCACTGCA CTCCAGCCTG GGCGACAGAG
    721 CGAGACTCCG TCTCAAAAAA AAAAAAAAAA AAAAAAATAC AAAAATTAGC CGGGCGTGGT
    781 GGCCCACGCC TGTAATCCCA GCTACTCGGG AGGCTAAGGC AGGAAAATTG TTTGAACCCA
    841 GGAGGTGGAG GCTGCAGTGA GCTGAGATTG TGCCACTTCA CTCCAGCCTG GGTGACAAAG
    901 TGAGACTCCG TCACAACAAC AACAACAAAA AGCTTCCCCA ACTAAAGCCT AGAAGAGCTT
    961 CTGAGGCGCT GCTTTGTCAA AAGGAAGTCT CTAGGTTCTG AGCTCTGGCT TTGCCTTGGC
   1021 TTTGCCAGGG CTCTGTGACC AGGAAGGAAG TCAGCATGCC TCTAGAGGCA AGGAGGGGAG
   1081 GAACACTGCA CTCTTAAGCT TCCGCCGTCT CAACCCCTCA CAGGAGCTTA CTGGCAAACA
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GENBANK ID: CAA72079.1
DEFINITION H.SAPIENS MRNA FOR ESTROGEN SULFOTRANSFERASE.
CDS 63..947
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    121 ATAAAGATTT TGTCAAATAT TGGGATAATG TGGAAGCGTT CCAGGCAAGA CCAGATGATC
    181 TTGTCATTGC CACCTACCCT AAATCTGGTA CAACCTGGGT TAGTGAAATT GTGTATATGA
    241 TCTATAAAGA GGGTGATGTG GAAAAGTGCA AAGAAGATGT AATTTTTAAT CGAATACCTT
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    661 GAAAAGAGGT GATAAAATTG ATACATTTCC TGGAAAGGAA GCCATCAGAG GAGCTTGTGG
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GENBANK ID: AAA63210.1
DEFINITION HUMAN KERATINOCYTE GROWTH FACTOR MRNA, COMPLETE CDS.
CDS 446..1030
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    181 AGTCAAATAG CAAACAGCGT CACAGCAACT GAACTTACTA CGAACTGTTT TTATGAGGAT
    241 TTATCAACAG AGTTATTTAA GGAGGAATCC TGTGTTGTTA TCAGGAACTA AAAGGATAAG
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1201 ACACTGCATT AAAGAAAGAT TTGAAAAGTA TACACAAAAA TCAGATTTAG TAACTAAAGG
1261 TTGTAAAAAA TTGTAAAACT GGTTGTACAA TCATGATGTT AGTAACAGTA ATTTTTTTCT
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1381 ATTCCTATCT GCTTATAAAA TGGCTGCTAT AATAATAATA ATACAGATGT TGTTATATAA
1441 GGTATATCAG ACCTACAGGC TTCTGGCAGG ATTTGTCAGA TAATCAAGCC ACACTAACTA
1501 TGGAAAATGA GCAGCATTTT AAATGCTTTC TAGTGAAAAA TTATAATCTA CTTAAACTCT
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1621 AAAAGTACAG GATTAGAACA TGCTTATACC TATAAATAAG AACAAAATTT CTAATGCTGC
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1741 CAGTGATTGA TGATAATACT GTACTTCATC TTACTTGCCA CAAAATAACA TTTTATAAAT
1801 CCTCAAAGTA AAATTGAGAA ATCTTTAAGT TTTTTTCAAG TAACATAATC TATCTTTGTA
1861 TAATTCATAT TTGGGAATAT GGCTTTTAAT AATGTTCTTC CCACAAATAA TCATGCTTTT
1921 TTCCTATGGT TACAGCATTA AACTCTATTT TAAGTTGTTT TTGAACTTTA TTGTTTTGTT
1981 ATTTAAGTTT ATGTTATTTA TAAAAAAAAA ACCTTAATAA GCTGTATCTG TTTCATATGC
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2161 ATAAGAGCCT GAAGCAATGC TTACAATAGA TGTCTCACAC AGAACAATAC AAATATGTAA
2221 AAACTCTTTC ACCACATATT CTTGCCAATT AATTGGATCA TATAAGTAAA ATCATTACAA
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2341 CATATTTTAA AACTATGTAT ATTTAAATTT AGTAATTTTC TAATCTCTAG AAATCTCTGC
2401 TGTTCAAAAG GTGGCAGCAC TGAAAGTTGT TTTCCTGTTA GATGGCAAGA GCACAATGCC
2461 CAAAATAGAA GATGCAGTTA AGAATAAGGG GCCCTGAATG TCATGAAGGC TTGAGGTCAG
2521 CCTACAGATA ACAGGATTAT TACAAGGATG AATTTCCACT TCAAAAGTCT TTCATTGGCA
2581 GATCTTGGTA GCACTTTATA TGTTCACCAA TGGGAGGTCA ATATTTATCT AATTTAAAAG
2641 GTATGCTAAC CACTGTGGTT TTAATTTCAA AATATTTGTC ATTCAAGTCC CTTTACATAA
2701 ATAGTATTTG GTAATACATT TATAGATGAG AGTTATATGA AAAGGCTAGG TCAACAAAAA
2761 CAATAGATTC ATTTAATTTT CCTGTGGTTG ACCTATACGA CCAGGATGTA GAAAACTAGA
2821 AAGAACTGCC CTTCCTCAGA TATACTCTTG GGAGAGAGCA TGAATGGTAT TCTGAACTAT
2881 CACCTGATTC AAGGACTTTG CTAGCTAGGT TTTGAGGTCA GGCTTCAGTA ACTGTAGTCT
2941 TGTGAGCATA TTGAGGGCAG AGGAGGACTT AGTTTTTCAT ATGTGTTTCC TTAGTGCCTA
3001 GCAGACTATC TGTTCATAAT CAGTTTTCAG TGTGAATTCA CTGAATGTTT ATAGACAAAA
3061 GAAAATACAC ACTAAAACTA ATCTTCATTT TAAAAGGGTA AAACATGACT ATACAGAAAT
3121 TTAAATAGAA ATAGTGTATA TACATATAAA ATACAAGCTA TGTTAGGACC AAATGCTCTT
3181 TGTCTATGGA GTTATACTTC CATCAAATTA CATAGCAATG CTGAATTAGG CAAAACCAAC
3241 ATTTAGTGGT AAATCCATTC CTGGTAGTAT AAGTCACCTA AAAAAGACTT CTAGAAATAT
3301 GTACTTTAAT TATTTGTTTT TCTCCTATTT TTAAATTTAT TATGCAAATT TTAGAAAATA
3361 AAATTTGCTC TAGTTACACA CCTTTAGAAT TCTAGAATAT TAAAACTGTA AGGGGCCTCC
3421 ATCCCTCTTA CTCATTTGTA GTCTAGGAAA TTGAGATTTT GATACACCTA AGGTCACGCA
3481 GCTGGGTAGA TATACAGCTG TCACAAGAGT CTAGATCAGT TAGCACATGC TTTCTACTCT
3541 TCGATTATTA GTATTATTAG CTAATGGTCT TTGGCATGTT TTTGTTTTTT ATTTCTGTTG
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3661 CAATGACTAA TCTATACTGT GATGATTTGA CTCAAAAGGA GAAAAGAAAT TATGTAGTTT
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3841 TCTAACAATT AGA
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GENBANK ID: AAA62202.1
DEFINITION HUMAN ENDOTHELIAL-MONOCYTE ACTIVATING POLYPEPTIDE II MRNA, COMPLETE CDS.
VERSION U10117.1 GI:498909
MRNA 1..1057
CDS 50..988
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 121 TCTTAAGCAG CAAGTTTCTC TACTTAAGGA GAAAGCAATT TTGCAGGCAA CTTTGAGGGA
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 241 AGAGCTAATT CAGGCAGAAA TTCAAAATGG AGTGAAGCAA ATAGCATTTC CATCTGGTAC
 301 TCCACTGCAC GCTAATTCTA TGGTTTCTGA AAATGTGATA CAGTCTACAG CAGTAACAAC
 361 CGTATCTTCT GGTACCAAAG AACAGATAAA AGGAGGAACA GGAGACGAAA AGAAAGCGAA
 421 AGAGAAAATT GAAAAGAAAG GAGAGAAGAA GGAGAAAAAA CAGCAATCAA TAGCTGGAAG
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 541 TGCTAGAAAA CACCCTGATG CAGATTCTTT GTATGTGGAA GAAGTAGATG TCGGAGAAAT
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1021 ACCTTAAAAG TAATAAAGAG AAATATATTT GTCACTT
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GENBANK ID: P17936
DEFINITION HUMAN ACIDIC FIBROBLAST GROWTH FACTOR MRNA, 5' END, CLONE LAMBDA-MJ36.
CDS 358..>478
/CODON_START=1

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 121 AGGACAAGTG GATCCAACAG CCTTCGCTCC AGGGGAATCA GGGCATCGCC TCCTTTTCTG
 181 GGAGGACACT CCCTTCTGAT GGTGAATGGG AACTCCCTTC CTCCTGCAGC AGCCTGCCTG
 241 CAGCTGTCCT GGTAGAACAG TGTGGACATT GCAGAAGCTG TCACTGCCCC AGAAAGAAAG
 301 CACCCCAGAG CCAAGGCAAA GAGTCTTGAA AGCGCCACAA GCAGCAGCTG CTGAGCCATG
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GENBANK ID: U76376.1
VERSION U76376.1 GI:1923234

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GENBANK ID: Y00638
VERSION Y00638.1 GI:34280

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GENBANK ID: AF001383.1
VERSION AF001383.1 GI:2199534

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GENBANK ID: XM_038595.3
VERSION XM_038595.3 GI:18590923

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GENBANK ID: M32292.1
VERSION M32292.1 GI:181492

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GENBANK ID: X06318
VERSION X06318.1 GI:35488

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GENBANK ID: J04132.1
VERSION J04132.1 GI:623041

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GENBANK ID: U04313.1
VERSION U04313.1 GI:453368

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GENBANK ID: X68968.1
VERSION X68968.1 GI:452315

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GENBANK ID: L03840.1
VERSION L03840.1 GI:182570

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RGTYTCLVENAVGSIRYNYLLDVLERSPHRPILQAGLPANTTAVVGSDVELLCKVYSD
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SLDLPLDPLWEFPRDRLVLGKPLGEGCFGQVVRAEAFGMDPARPDQASTVAVKMLKDN
ASDKDLADLVSEMEVMKLIGRHKNIINLLGVCTQEGPLYVIVECAAKGNLREFLRARR
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GENBANK ID: AF043342.1
VERSION AF043342.1 GI:2905633

VRSSSRTPSDKPVAHVVANPQAEGQLQWLNRRANALLANGVELR
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GENBANK ID: NM_000735.2
VERSION NM_000735.2 GI:10800407

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GENBANK ID: M83533.1
VERSION M83533.1 GI:178541

LRKHNIETYLIKQPEDSLLSLPEDIVKESVSSSDRRNSGATFTE
GSWSPELPFDNIVGKQNTLAALTRNSINLLPNHLAQALHVQSGPEEINKRIEHTIDLR
SGDKLRREHIKPFSLMFKDSSLEHKYSQMRDEVFKSNLVCAFIVLLFITAIQSLLPSS
RVMPMTIQFSILIMLHSALVLITTAEDYKCLPLILRKTCCWINETYLARNVIIFASIL
INFLGAILNILWCDFDKSIPLKNLTFNSSAVFTDICSYPEYFVFTGVLAMVTCAVFLR
LNSVLKLAVLLIMIAIYALLTETVYAGLFLRYDNLNHSGEDFLGTKEVSLLLMAMFLL
AVFYHGQQLEYTARLDFLWRVQAKEEINEMKELREHNENMLRNILPSHVARHFLEKDR
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GENBANK ID: M31767.1
VERSION M31767.1 GI:181615

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GENBANK ID: X14723

VERSION X14723.1 GI:30250

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NETMMALWEECKPCLKQTCMKFYARVCRSGSGLVGRQLEEFLNQSSPFYFWMNGDRID
SLLENDRQQTHMLDVMQDHFSRASSIIDELFQDRFFTREPQDTYHYLPFSLPHRRPHF
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GENBANK ID: X04391.1
VERSION X04391.1 GI:37186

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GENBANK ID: S78187.1
VERSION S78187.1 GI:243485

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GENBANK ID: Y00096.1
VERSION Y00096.1 GI:30455

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GENBANK ID: XM_055551.3
VERSION XM_055551.3 GI:18557356

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GENBANK ID: M84711.1
VERSION M84711.1 GI:182774

MAVGKNKRLTKGGKKGAKKKVVDPFSKKDWYDVKAPAMFNIRNI
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GENBANK ID: X53505
VERSION X53505.1 GI:36145

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GENBANK ID: X06617
VERSION X06617.1 GI:36143

MADIQTERAYQKQPTIFQNKKRVLLGETGKEKLPRYYKNIGLGF
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GENBANK ID: M55040.1
VERSION M55040.1 GI:177974

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GENBANK ID: NM_000717.2
VERSION NM_000717.2 GI:9951925

MRMLLALLALSAARPSASAESHWCYEVQAESSNYPCLVPVKWGG
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GENBANK ID: S70587.1

VERSION S70587.1 GI:546848

MTALFLMSMLFGLACGQAMSFCIPTEYTMHIERRECAYCLTINT
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GENBANK ID: M34057
VERSION M34057.1 GI:339547

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PSSCIDGQCVNTEGSYNCFCTHPMVLDASEKRCIRPAESNEQIEETDVYQDLCWEHLS
DEYVCSRPLVGKQTTYTECCCLYGEAWGMQCALCPLKDSDDYAQLCNIPVTGRRQPYG
RDALVDFSEQYTPEADPYFIQDRFLNSFEELQAEECGILNGCENGRCVRVQEGYTCDC
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GENBANK ID: AF257099.1
VERSION AF257099.1 GI:8037944

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GENBANK ID: L06505.1
VERSION L06505.1 GI:186799

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GENBANK ID: X79234.1
VERSION X79234.1 GI:495125

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GENBANK ID: X59932.1
VERSION X59932.1 GI:30255

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GENBANK ID: AAA98616.1
VERSION AAA98616.1 GI:178428

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  1 MQGPWVLLLL GLRLQLSLGI IPVEEENPDF WNRQAAEALG AAKKLQPAQT AAKNLIMFLG
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121 GVKGNFQTIG LSAAARFNQC NTTRGNEVIS VVNRAKKAGK SVGVVTTTRV QHASPAGTYA
181 HTVNRNWYSD ADVPASARQE GCQDIATQLI SNMDIDVILG GGRKYMFPMG TPDPEYPDDY
241 SQGGTRLDGK NLVQEWLAKH QGARYVWNRT ELLQASLDPS VTHLMGLFEP GDMKYEIHRD
301 STLDPSLMEM TEAALLLLSR NPRGFFLFVE GGRIDHGHHE SRAYRALTET IMFDDAIERA
361 GQLTSEEDTL SLVTADHSHV FSFGGYPLRG SSIFGLAPGK ARDRKAYTVL LYGNGPGYVL
421 KDGARPDVTE SESGSPEYRQ QSAVPLDGET HAGEDVAVFA RGPQAHLVHG VQEQTFIAHV
481 MAFAACLEPY TACDLAPPAG TTDAAHPGPS VVPALLPLLA GTLLLLGTAT AP
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GENBANK ID: XM_041507.1
VERSION XM_041507.1 GI:14737457

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VTAIIFCVALSAYDLVLAEDEEMNRMHESMKLFDSICNNKWFTDTSIILFLNKKDLFE
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GENBANK ID: NM_001032.2
VERSION NM_001032.2 GI:13904868

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GENBANK ID: M22430.1
VERSION M22430.1 GI:190888

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GENBANK ID: X63527
VERSION X63527.1 GI:36127

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GENBANK ID: AF099644.1
VERSION AF099644.1 GI:4323527

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GENBANK ID: X51466
VERSION X51466.1 GI:31105

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VEAKNPADLPKLVEGLKRLAKSDPMVQCIIEESGEHIIAGAGELHLEICLKDLEEDHA
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GENBANK ID: M15661
VERSION M15661.1 GI:337577

MVNVPKTRRTFCKKCGKHQPHKVTQYKKGKDSLYAQGRRRYDRK
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VIQF

GENBANK ID: J04823.1
VERSION J04823.1 GI:1311703

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GENBANK ID: NM_001760.2
VERSION NM_001760.2 GI:16950657

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GPSQTSTPTDVTAIHL

GENBANK ID: NM_002625.1
DEFINITION HOMO SAPIENS 6-PHOSPHOFRUCTO-2-KINASE/FRUCTOSE-2,6-BIPHOSPHATASE 1 (PFKFB1), MRNA.
VERSION NM_002625.1 GI:4505744
CDS 80..1495

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 241 CAAGACCTAT ATCTCCACAA AGCTCACACG ATATCTCAAC TGGATAGGAA CACCAACTAA
 301 AGTGTTTAAT TTAGGCCAGT ATCGACGAGA GGCAGTGAGC TACAAGAACT ATGAATTCTT
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1201 TCTGGAGCCA GTGATAATGG AGCTAGAACG ACAGGAGAAT GTACTGGTGA TCTGCCACCA
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1381 GGAATCCATC TACCTGAATG TGGAGGCCGT GAACACACAC CGGGAGAAGC CTGAGAATGT
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1501 TTCCAAGAAG TCAAACTGCC TGTGTCCTCA TCGCCTTCCA CCTTTAGGAA ATGCTATCTT
1561 TGCTCTTCTC CTACTCTGCC TTGGCCTCAC TGAGGCACCC CACTTCCAGT GAAGAAGTCC
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GENBANK ID: D00760
DEFINITION HUMAN MRNA FOR PROTEASOME SUBUNIT HC3.
VERSION D00760.1 GI:220023
CDS 1..705
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      301 TACCAAGAAC CCATTCCTAC AGCTCAGCTG GTACAGAGAG TAGCTTCTGT GATGCAAGAA
      361 TATACTCAGT CAGGTGGTGT TCGTCCATTT GGAGTTTCTT TACTTATTTG TGGTTGGAAT
      421 GAGGGACGAC CATATTTATT TCAGTCAGAT CCATCTGGAG CTTACTTTGC CTGGAAAGCT
      481 ACAGCAATGG GAAAGAACTA TGTGAATGGG AAGACTTTCC TTGAGAAAAG ATATAATGAA
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      601 GGGCAAATGA CAGAGGATAA CATAGAAGTT GGAATCTGCA ATGAAGCTGG ATTTAGGAGG
      661 CTTACTCCAA CTGAAGTTAA GGATTACTTG GCTGCCATAG CATAACAATG AAGTGACTGA
      721 AAAATCCAGA ATTTCAGATA ATCTATCTAC TTAAACATGT TTAAAGTATG TTTTGTTTTG
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GENBANK ID: P10644

GENBANK ID: XM_043948.2
DEFINITION HOMO SAPIENS ALDOLASE A, FRUCTOSE-BISPHOSPHATE (ALDOA), MRNA.
VERSION XM_043948.2 GI:18585537
CDS 243..1349
/CODON_START=1

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      661 AGGACGGAGC TGACTTCGCC AAGTGGCGTT GTGTGCTGAA GATTGGGGAA CACACCCCCT
      721 CAGCCCTCGC CATCATGGAA AATGCCAATG TTCTGGCCCG TTATGCCAGT ATCTGCCAGC
      781 AGGTGGGCCT GCAGAATGGC ATTGTGCCCA TCGTGGAGCC TGAGATCCTC CCTGATGGGG
      841 ACCATGACTT GAAGCGCTGC CAGTATGTGA CCGAGAAGGT GCTGGCTGCT GTCTACAAGG
      901 CTCTGAGTGA CCACCACATC TACCTGGAAG GCACCTTGCT GAAGCCCAAC ATGGTCACCC
      961 CAGGCCATGC TTGCACTCAG AAGTTTTCTC ATGAGGAGAT TGCCATGGCG ACCGTCACAG
     1021 CGCTGCGCCG CACAGTGCCC CCCGCTGTCA CTGGGATCAC CTTCCTGTCT GGAGGCCAGA
     1081 GTGAGGAGGA GGCGTCCATC AACCTCAATG CCATTAACAA GTGCCCCCTG CTGAAGCCCT
     1141 GGGCCCTGAC CTTCTCCTAC GGCCGAGCCC TGCAGGCCTC TGCCCTGAAG GCCTGGGGCG
     1201 GGAAGAAGGA GAACCTGAAG GCTGCGCAGG AGGAGTATGT CAAGCGAGCC CTGGCCAACA
     1261 GCCTTGCCTG TCAAGGAAAG TACACTCCGA GCGGTCAGGC TGGGGCTGCT GCCAGCGAGT
     1321 CCCTCTTCGT CTCTAACCAC GCCTATTAAG CGGAGGTGTT CCCAGGCTGC CCCCAACACT
     1381 CCAGGCCCTG CCCCCTCCCA CTCTTGAAGA GGAGGCCGCC TCCTCGGGGC TCCAGGCTGG
     1441 CTTGCCCGCG CTCTTTCTTC CCTCGTGACA GTGGTGTGTG GTGTCGTCTG TGAATGCTAA
     1501 GTCCATCACC CTTTCCGGCA CACTGCCAAA TAAACAGCTA TTTAAGGGGG
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GENBANK ID: NM_005175.1
DEFINITION HOMO SAPIENS ATP SYNTHASE, H+ TRANSPORTING, MITOCHONDRIAL F0 COMPLEX, SUBUNIT C (SUBUNIT 9), ISOFORM 1 (ATP5G1), MRNA.
VERSION NM_005175.1 GI:4885080
CDS 120..530
/CODON_START=1

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        1 GGGGAAGCTG AGGGCTGAGA CCAAGGGCTA AAGCTGGGAG GTGAGTCTGT CACCTTGAGC
       61 CGGGCGAGCG CTGTGGGCCA AGCAGGGGTT GCAGGGCAGT AGGAGTGCAG ACTGAAAAAA
      121 TGCAGACCGC CGGGGCATTA TTCATTTCTC CAGCTCTGAT CCGCTGTTGT ACCAGGGGTC
      181 TAATCAGGCC TGTGTCTGCC TCCTTCTTGA ATAGCCCAGT GAATTCATCT AAACAGCCTT
      241 CCTACAGCAA CTTCCCACTC CAGGTGGCCA GACGGGAGTT CCAGACCAGT GTTGTCTCCC
      301 GGGACATTGA CACAGCAGCC AAGTTTATTG GTGCTGGGGC AGCCACAGTT GGTGTGGCTG
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       361 GTTCAGGGGC TGGCATTGGA ACCGTGTTTG GCAGCTTGAT CATTGGCTAT GCCAGGAACC
       421 CGTCTCTCAA GCAGCAGCTC TTCTCCTATG CCATTCTTGG CTTTGCCCTG TCTGAGGCCA
       481 TGGGGCTTTT CTGTTTGATG GTCGCCTTCC TCATCCTCTT CGCCATGTGA GGCTCCATGG
       541 GGGGTCACCG GCCTGTTGCT ACTGCAACTC CACACCATTC TTGGTGCTGG GGTGTGTTAA
       601 GCTTTACCAT TAAACACAAC GTTTCTCTAA A
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GENBANK ID: M20496.1
DNA     LINEAR
DEFINITION  HUMAN CATHEPSIN L GENE, COMPLETE CDS.
VERSION     M20496.1  GI:809235
CDS             134..1135
/CODON_START=1

         1 ACCTCCACGT GCCCTGTTTT TCTGGAGGCA CATCCTTGGC CTCTTCCACA GTCCTTGGGT
        61 AAATGCTTGG GAGAATAATT TAAATATTTT TATTCTACCA TGGTGGCCCT AATTTTTCAG
       121 GGGGCAGTAA GATATGAATC CTACACTCAT CCTTGCTGCC TTTTGCCTGG GAATTGCCTC
       181 AGCTACTCTA ACATTTGATC ACAGTTTAGA GGCACAGTGG ACCAAGTGGA AGGCGATGCA
       241 CAACAGATTA TACGGCATGA ATGAAGAAGG ATGGAGGAGA GCAGTGTGGG AGAAGAACAT
       301 GAAGATGATT GAACTGCACA ATCAGGAATA CAGGGAAGGG AAACACAGCT TCACAATGGC
       361 CATGAACGCC TTTGGAGACA TGACCAGTGA AGAATTCAGG CAGGTGATGA ATGGCTTTCA
       421 AAACCGTAAG CCCAGGAAGG GGAAAGTGTT CCAGGAACCT CTGTTTTATG AGGCCCCCAG
       481 ATCTGTGGAT TGGAGAGAGA AAGGCTACGT GACTCCTGTG AAGAATCAGG GTCAGTGTGG
       541 TTCTTGTTGG GCTTTTAGTG CTACTGGTGC TCTTGAAGGA CAGATGTTCC GGAAAACTGG
       601 GAGGCTTATC TCACTGAGTG AGCAGAATCT GGTAGACTGC TCTGGGCCTC AAGGCAATGA
       661 AGGCTGCAAT GGTGGCCTAA TGGATTATGC TTTCCAGTAT GTTCAGGATA ATGGAGGCCT
       721 GGACTCTGAG GAATCCTATC CATATGAGGC AACAGAAGAA TCCTGTAAGT ACAATCCCAA
       781 GTATTCTGTT GCTAATGACA CCGGCTTTGT GGACATCCCT AAGCAGGAGA AGGCCCTGAT
       841 GAAGGCAGTT GCAACTGTGG GGCCCATTTC TGTTGCTATT GATGCAGGTC ATGAGTCCTT
       901 CCTGTTCTAT AAAGAAGGCA TTTATTTTGA GCCAGACTGT AGCAGTGAAG ACATGGATCA
       961 TGGTGTGCTG GTGGTTGGCT ACGGATTTGA AAGCACAGAA TCAGATAACA ATAAATATTG
      1021 GCTGGTGAAG AACAGCTGGG GTGAAGAATG GGGCATGGGT GGCTACGTAA AGATGGCCAA
      1081 AGACCGGAGA AACCATTGTG GAATTGCCTC AGCAGCCAGC TACCCCACTG TGTGAGCTGT
      1141 GGACGGTGAT GAGGAAGGAC TTGACTGGGG ATGGCGCATG CATGGGAGGA ATTCTTCAGT
      1201 CTACCAGCCC CCGCTGTGTC GGATACACAC TCGAATCATT GAAGATCCGA GTGTGATTTG
      1261 AATTCTGTGA TATTTTCACA CTGGTAAATG TTACCTCTAT TTTAATTACT GCTATAAATA
      1321 GGTTTATATT ATTGATTCAC TTACTGACTT TGCATTTTCG TTTTTAAAAG GATGTATAAA
      1381 TTTTTACCTG TTTAAATAAA ATCG
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GENBANK ID:  XM_031596.3
DEFINITION  HOMO SAPIENS ANNEXIN A4 (ANXA4), MRNA.
VERSION     XM_031596.3  GI:18553329
CDS             48..770
/CODON_START=1

         1 GAAGAACTTC TGCTTGGGTG GCTGAACTCT GATCTTGACC TAGAGTCATG GCCATGGCAA
        61 CCAAAGGAGG TACTGTCAAA GCTGCTTCAG GATTCAATGC CATGGAAGAT GCCCAGACCC
       121 TGAGGAAGGC CATGAAAGGG CTCGGCACCG ATGAAGACGC CATTATTAGC GTCCTTGCCT
       181 ACCGCAACAC CGCCCAGCGC CAGGAGATCA GGACAGCCTA CAAGAGCACC ATCGGCAGGG
       241 ACTTGATAGA CGACCTGAAG TCAGAACTGA GTGGCAACTT CGAGCAGGTG ATTGTGGGGA
       301 TGATGACGCC CACGGTGCTG TATGACGTGC AAGAGCTGCG AAGGGCCATG AAGGGAGCCG
       361 GCACTGATGA GGGCTGCCTA ATTGAGATCC TGGCCTCCCG GACCCCTGAG GAGATCCGGC
       421 GCATAAGCCA AACCTACCAG CAGCAATATG GACGGAGCCT TGAAGATGAC ATTCGCTCTG
       481 ACACATCGTT CATGTTCCAG CGAGTGCTGG TGTCTCTGTC AGCTGGTGGG AGGGATGAAG
       541 GAAATTATCT GGACGATGCT CTCGTGAGAC AGGATGCCCA GGACCTGTAT GAGGCTGGAG
       601 AGAAGAAATG GGGGACAGAT GAGGTGAAAT TTCTAACTGT TCTCTGTTCC CGGAACCGAA
       661 ATCACCTGTT GCATGGTTTG ATGAATACAA AAGGATATCA CAGAAGGATA TTGAACAGAG
       721 TATTAAATCT GAAACATCTG GTAGCTTTGA AGATGCTCTG CTGGCTATAG TAAAGTGCAT
       781 GAGGAACAAA TCTGCATATT TTGCTGAAAA GCTCTATAAA TCGATGAAGG GCTTGGGCAC
       841 CGATGATAAC ACCCTCATCA GAGTGATGGT TTCTCGAGCA GAAATTGACA TGTTGGATAT
       901 CCGGGCACAC TTCAAGAGAC TCTATGGAAA GTCTCTGTAC TCGTTCATCA AGGGTGACAC
       961 ATCTGGAGAC TACAGGAAAG TACTGCTTGT TCTCTGTGGA GGAGATGATT AAAATAAAAA
      1021 TCCCAGAAGG ACAGGAGGAT TCTCAACACT TTGAATTTTT TTAACTTCAT TTTTCTACAC
      1081 TGCTATTATC ATTATCTCAG AATGCTTATT TCCAATTAAA ACGCCTACAG CTGCCTCCTA
      1141 GAATATAGAC TGTCTGTATT ATTATTCACC TATAATTAGT CATTATGATG CTTTAAAGCT
      1201 GTACTTGCAT TTCAAAGCTT ATAAGATATA AATGGAGATT TTAAAGTAGA AATAAATATG
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1261 TATTCCATGT TTTTAAAAGA TTACTTTCTA CTTTGTGTTT CACAGACATT GAATATATTA
1321 AATTATTCCA TATTTTCTTT TCAGTGAAAA ATTTTTTAAA TGGAAGACTG TTCTAAAATC
1381 ACTTTTTTCC CTAATCCAAT TTTTAGAGTG GCTAGTAGTT TCTTCATTTG AAATTGTAAG
1441 CATCCGGTCA GTAAGAATGC CCATCCAGTT TTCTATATTT CATAGTCAAA GCCTTGAAAG
1501 CATCTACAAA TCTCTTTTTT TAGGTTTTGT CCATAGCATC AGTTGATCCT TACTAAGTTT
1561 TTCATGGGAG ACTTCCTTCA TCACATCTTA TGTTGAAATC ACTTTCTGTA GTCAAAGTAT
1621 ACCAAAACCA ATTTATCTGA ACTAAATTCT AAAGTATGGT TATACAAACC ATATACATCT
1681 GGTTACCAAA CATAAATGCT GAACATTCCA TATTATTATA GTTAATGTCT TAATCCAGCT
1741 TGCAAGTGAA TGGAAAAAAA AATAAGCTTC AAACTAGGTA TTCTGGGAAT GATGTAATGC
1801 TCTGAATTTA GTATGATATA AAGAAAACTT TTTTGTGCTA AAAATACTTT TTAAAATCAA
1861 TTTTGTTGAT TGTAGTAATT TCTATTTGCA CTGTGCCTTT CAACTCCAGA AACATTCTGA
1921 AGATGTACTT GGATTTAATT AAAAAGTTCA CTTTGT
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GENBANK ID: M22865.1
DEFINITION HUMAN CYTOCHROME B5 MRNA, COMPLETE CDS.
VERSION M22865.1 GI:181226

53..457
CODON_START=1

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   1 CAGCCAGCTC GACGGGGCTG TGTGTGCTGG GCCTGGCTCG CGGCGAACCG AGATGGCAGA
  61 GCAGTCGGAC GAGGCCGTGA AGTACTACAC CCTAGAGGAG ATTCAGAAGC ACAACCACAG
 121 CAAGAGCACC TGGCTGATCC TGCACCACAA GGTGTACGAT TTGACCAAAT TTCTGGAAGA
 181 GCATCCTGGT GGGGAAGAAG TTTTAAGGGA ACAAGCTGGA GGTGACGCTA CTGAGAACTT
 241 TGAGGATGTC GGGCACTCTA CAGATGCCAG GGAAATGTCC AAAACATTCA TCATTGGGGA
 301 GCTCCATCCA GATGACAGAC CAAAGTTAAA CAAGCCTCCG GAAACTCTTA TCACTACTAT
 361 TGATTCTAGT TCCAGTTGGT GGACCAACTG GGTGATCCCT GCCATCTCTG CAGTGGCCGT
 421 CGCCTTGATG TATCGCCTAT ACATGGCAGA GGACTGAACA CCTCCTCAGA AGTCAGCGCA
 481 GGCCGAGCCT GCTTTGGACA CGGGAGAAAA GAAGCCATTG CTAACTACTT CAACTGACAG
 541 AAACCTTCAC TTGAAAACAA TGATTTTAAT ATATCTCTTT CTTTTTCTTC CGACATTAGA
 601 AACAAAACAA AAAGAACTGT CCTTTCTGCG CTCAAATTTT TCGAGTGTGC CTTTTTATTC
 661 ATCTACTTTA TTTTGATGTT TCCTTAATGT GTAATTTACT TATTATAAGC ATGATCTTTT
 721 AAAAATATAT TTGGCTTTTA AAG
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GENBANK ID: M14362.1
DEFINITION HUMAN T-CELL SURFACE ANTIGEN CD2 (T11) MRNA, COMPLETE CDS.
VERSION M14362.1 GI:179133
CDS 10..1065
/CODON_START=1

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   1 ACCCCTAAGA TGAGCTTTCC ATGTAAATTT GTAGCCAGCT TCCTTCTGAT TTTCAATGTT
  61 TCTTCCAAAG GTGCAGTCTC CAAAGAGATT ACGAATGCCT TGGAAACCTG GGGTGCCTTG
 121 GGTCAGGACA TCAACTTGGA CATTCCTAGT TTTCAAATGA GTGATGATAT TGACGATATA
 181 AAATGGGAAA AAACTTCAGA CAAGAAAAAG ATTGCACAAT TCAGAAAAGA GAAAGAGACT
 241 TTCAAGGAAA AAGATACATA TAAGCTATTT AAAAATGGAA CTCTGAAAAT TAAGCATCTG
 301 AAGACCGATG ATCAGGATAT CTACAAGGTA TCAATATATG ATACAAAAGG AAAAAATGTG
 361 TTGGAAAAAA TATTTGATTT GAAGATTCAA GAGAGGGTCT CAAAACCAAA GATCTCCTGG
 421 ACTTGTATCA ACACAACCCT GACCTGTGAG GTAATGAATG GAACTGACCC CGAATTAAAC
 481 CTGTATCAAG ATGGGAAACA TCTAAAACTT TCTCAGAGGG TCATCACACA CAAGTGGACC
 541 ACCAGCCTGA GTGCAAAATT CAAGTGCACA GCAGGGAACA AAGTCAGCAA GGAATCCAGT
 601 GTCGAGCCTG TCAGCTGTCC AGAGAAAGGT CTGGACATCT ATCTCATCAT TGGCATATGT
 661 GGAGGAGGCA GCCTCTTGAT GGTCTTTGTG GCACTGCTCG TTTTCTATAT CACCAAAAGG
 721 AAAAAACAGA GGAGTCGGAG AAATGATGAG GAGCTGGAGA CAAGAGCCCA CAGAGTAGCT
 781 ACTGAAGAAA GGGGCCGGAA GCCCCACCAA ATTCCAGCTT CAACCCCTCA GAATCCAGCA
 841 ACTTCCCAAC ATCCTCCTCC ACCACCTGGT CATCGTTCCC AGGCACCTAG TCATCGTCCC
 901 CCGCCTCCTG GACACCGTGT TCAGCACCAG CCTCAGAAGA GGCCTCCTGC TCCGTCGGGC
 961 ACACAAGTTC ACCAGCAGAA AGGCCCGCCC CTCCCCAGAC CTCGAGTTCA GCCAAAACCT
1021 CCCCATGGGG CAGCAGAAAA CTCATTGTCC CCTTCCTCTA ATTAAAAAAG ATAGAAACTG
1081 TATTTTTCAA TAAAAAGCAC TGTGGATTTC TGCCCTCCTG ATGTGCATAT CCGTACTTCC
1141 ATGAGGTGTT TTCTGTGTGC AGAACATTGT CACCTCCTGA GGCTGTGGGC CACAGCCACC
1201 TCTGCATCTT CGAACTCAGC CATGTGGTCA ACATCTGGAG TTTTTGGTCT CCTCAGAGAG
1261 CTCCATCACA CCAGTAAGGA GAAGCAATAT AAGTGTGATT GCAAGAATGG TAGAGGACCG
1321 AGCACAGAAA TCTTAGAGAT TTCCTGTCCC CTCTCAGGTC ATGTGTAGAT GCGATAAATC
1381 AAGTGATTGG TGTGCCTGGG TCTCACTACA AGCAGCCTAT CTGCTTAAGA GACTCTGGAG
1441 TTTCTTATGT GCCCTGGTGG ACACTTGCCC ACCATCCTGT GAGTAAAAGT GAAATAAAAG
1501 CTTTGACTAG
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GENBANK ID: XM_087746.1
DEFINITION HOMO SAPIENS SIMILAR TO KIDNEY AMINOPEPTIDASE M; LEUCINE ARYLAMINOPEPTIDASE 1 (LOC153726), MRNA.
VERSION XM_087746.1 GI:18561749
CDS 262..639
/CODON_START=1

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   1 GAGTTCCATG CCACCTCCCC GCCCTTTACA GACATGCTAT AAGGTCCCCA GCCCAGTCAC
  61 TCCGCAGTGC CTCTCTCTTC CTCCCCATGG ACTATACACA GGCCCTGCTT GTCCTGGAGG
 121 AAAGTTTGGA CGTCATTATA TAGATCAGGA GACTGAAGTA CTGAAAGGTT AAATGACTTG
 181 CCAAAGAATG AGATCTTTTT TTCTAACATT TTACATAATA TCCTCAGAGA AGATCACGCC
 241 CTGGTGACTA GAGCTGTGGC CATGAAGGTG GAAAATTTCA AAACAAGTGA AATACAGGAA
 301 CTCTTTGACA TATTTACTTA CAGCAAGGGA GCGTCTATGG CCCGGATGCT TTCTTGTTTC
 361 TTGAATGAGC ATTTATTTGT CAGTGCACTC AAGTCATATT TGAAGACATT TTCCTACTCA
 421 AACGCTGAGC AAGATGATCT ATGGAGGCAT TTTCAAATGG CCATAGATGA CCAGAGTACA
 481 GTTATTTTGC CAGCAACAAT AAAAAACATA ATGGACAGTT GGACACACCA GAGTGGTTTT
 541 CCAGTGATCA CTTTAAATGT GTCTACTGGC GTCATGAAAC AGGAGCCATT TTATCTTGAA
 601 AACATTAAAA ATCGGACTCT TCTAACCAGC AATAAGTGAC ACATGGATTG TCCCTATTCT
 661 TTGGATAAAA AATGGAACTA CACAACCTTT AGTCTGGCTA GA
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GENBANK ID: P31749
DEFINITION DICTYOSTELIUM DISCOIDEUM RAC-ALPHA SERINE/THREONINE KINASE HOMOLOG MRNA, COMPLETE CDS.
VERSION U15210.1 GI:1000068
CDS 1..1335
/CODON_START=1

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   1 ATGTCAACAG CACCAATTAA ACATGAAGGT TTCCTCACTA AAGAAGGTGG TGGTTTCAAA
  61 AGTTGGAAAA AGAGATGGTT CATTCTCAAA GGTGGTGATT TAAGTTATTA TAAAACAAAA
 121 GGTGAACTTG TACCATTAGG AGTTATTCAT TTAAATACAT CAGGTCATAT TAAAAATTCT
 181 GATCGTAAGA AAAGAGTTAA TGGATTTGAA GTACAAACAC CATCACGTAC ATATTTCTTA
 241 TGTTCAGAGA CAGAGGAAGA ACGTGCAAAA TGGATAGAGA TATTAATTAA TGAAAGAGAA
 301 TTATTATTGA ATGGTGGTAA ACAACCAAAG AAATCGGAAA AGGTAGGAGT TGCAGATTTT
 361 GAATTATTGA ATTTAGTTGG TAAAGGTAGT TTTGGTAAAG TTATTCAAGT TAGAAAGAAA
 421 GATACTGGTG AAGTGTATGC AATGAAAGTT TTATCAAAGA AACATATCGT AGAGCATAAC
 481 GAAGTCGAAC ATACATTGAG TGAGCGTAAT ATTCTTCAAA AGATCAATCA CCCATTTTTG
 541 GTTAATCTCA ACTACAGTTT TCAAACAGAG GATAAGCTTT ACTTTATCTT GGATTATGTT
 601 AATGGTGGTG AGTTATTCTA TCATCTTCAA AAGGACAAAA AGTTTACAGA GGATCGTGTC
 661 CGTTATTATG GCGCAGAGAT CGTATTGGCA TTGGAACATT TACATTTGTC GGGTGTCATC
 721 TATAGAGATT TGAAACCAGA GAATTTACTA CTCACCAACG AGGGTCACAT TTGCATGACC
 781 GATTTCGGTC TTTGCAAAGA GGGTCTATTG ACACCAACCG ACAAAACTGG TACTTTCTGT
 841 GGTACTCCTG AATATTTAGC ACCCGAAGTA CTTCAAGGCA ATGGTTATGG TAAACAAGTG
 901 GATTGGTGGA GTTTTGGTTC TCTCCTCTAT GAAATGCTCA CTGGTTTACC ACCATTCTAC
 961 AATCAAGACG TCCAAGAGAT GTATCGTAAG ATCATGATGG AGAAATTATC TTTCCCACAT
1021 TTCATTTCTC CAGATGCTCG TTCCCTCTTG GAACAACTCT TGGAAAGAGA TCCTGAAAAA
1081 AGACTTGCCG ATCCAAATCT TATTAAAAGA CATCCTTTCT TCCGTTCCAT CGATTGGGAA
1141 CAATTATTCC AAAAGAATAT TCCACCACCA TTCATTCCAA ATGTTAAAGG TTCTGCTGAT
1201 ACCTCTCAAA TTGATCCAGT TTTCACTGAT GAAGCTCCTT CTTTAACTAT GGCTGGTGAA
1261 TGTGCTTTAA ATCCGCAACA ACAAAAAGAT TTTGAAGGAT TTACATATGT CGCTGAATCT
1321 GAACATTTAA GATAA
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GENBANK ID: NM_000102.2
DEFINITION HOMO SAPIENS CYTOCHROME P450, SUBFAMILY XVII (STEROID 17-ALPHA-HYDROXYLASE), ADRENAL HYPERPLASIA (CYP17), MRNA.
VERSION NM_000102.2 GI:13904854
CDS 61..1587

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   1 GAGTTGCCAC AGCTCTTCTA CTCCACTGCT GTCTATCTTG CCTGCCGGCA CCCAGCCACC
  61 ATGTGGGAGC TCGTGGCTCT CTTGCTGCTT ACCCTAGCTT ATTTGTTTTG GCCCAAGAGA
 121 AGGTGCCCTG GTGCCAAGTA CCCCAAGAGC CTCCTGTCCC TGCCCCTGGT GGGCAGCCTG
 181 CCATTCCTCC CCAGACATGG CCATATGCAT AACAACTTCT TCAAGCTGCA GAAAAAATAT
 241 GGCCCCATCT ATTCTGTTCG TATGGGCACC AAGACTACAG TGATTGTCGG CCACCACCAG
 301 CTGGCCAAGG AGGTGCTTAT TAAGAAGGGC AAGGACTTCT CTGGGCGGCC TCAAATGGCA
 361 ACTCTAGACA TCGCGTCCAA CAACCGTAAG GGTATCGCCT TCGCTGACTC TGGCGCACAC
 421 TGGCAGCTGC ATCGAAGGCT GGCGATGGCC ACCTTTGCCC TGTTCAAGGA TGGCGATCAG
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 481 AAGCTGGAGA AGATCATTTG TCAGGAAATC AGTACATTGT GTGATATGCT GGCCACCCAC
 541 AACGGACAGT CCATAGACAT CTCCTTTCCT GTCTTCGTGG CGGTAACCAA TGTCATCTCC
 601 TTGATCTGCT TCAATACCTC CTACAAGAAT GGGGACCCTG AGTTGAATGT CATACAGAAT
 661 TACAATGAAG GCATCATAGA CAACCTGAGC AAAGACAGCC TGGTGGACCT AGTCCCCTGG
 721 TTGAAGATTT TCCCCAACAA AACCCTGGAA AAATTAAAGA GCCATGTTAA AATACGAAAT
 781 GATCTGCTGA ATAAAATACT TGAAAATTAC AAGGAGAAAT TCCGGAGTGA CTCTATCACC
 841 AACATGCTGG ACACACTGAT GCAAGCCAAG ATGAACTCAG ATAATGGCAA TGCTGGCCCA
 901 GATCAAGATT CAGAGCTGCT TTCAGATAAC CACATTCTCA CCACCATAGG GGACATCTTT
 961 GGGGCTGGCG TGGAGACCAC CACCTCTGTG GTTAAATGGA CCCTGGCCTT CCTGCTGCAC
1021 AATCCTCAGG TGAAGAAGAA GCTCTACGAG GAGATTGACC AGAATGTGGG TTTCAGCCGC
1081 ACACCAACTA TCAGTGACCG TAACCGTCTC CTCCTGCTGG AGGCCACCAT CCGAGAGGTG
1141 CTTCGCCTCA GGCCCGTGGC CCCTATGCTC ATCCCCCACA AGGCCAACGT TGACTCCAGC
1201 ATCGGTGAGT TTGCTGTGGA CAAGGGCACA GAAGTTATCA TCAATCTGTG GGCGCTGCAT
1261 CACAATGAGA AGGAGTGGCA CCAGCCGGAT CAGTTCATGC CTGAGCGTTT CTTGAATCCA
1321 GCGGGGACCC AGCTCATCTC ACCGTCAGTA AGCTATTTGC CCTTCGGAGC AGGACCTCGC
1381 TCCTGTATAG GTGAGATCCT GGCCCGCCAG GAGCTCTTCC TCATCATGGC CTGGCTGCTG
1441 CAGAGGTTCG ACCTGGAGGT GCCAGATGAT GGGCAGCTGC CCTCCCTGGA AGGCATCCCC
1501 AAGGTGGTCT TTCTGATCGA CTCTTTCAAA GTGAAGATCA AGGTGCGCCA GGCCTGGAGG
1561 GAAGCCCAGG CTGAGGGTAG CACCTAAAGG CTGTAACTCA CAGCCCCTGT CCACCCTATG
1621 TGGCCCCACA ACACAGATTT AGAGATACAA CCCCCCACCC TTCTCCGCCA TTCTTCCCTA
1681 CTCCCAACCC ACTCTGCCTT CTTTTTCAGC TTGTGGCAAT GCCAGTGATG TGCATAAACA
1741 GTTTTTTTTT TTTCC
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GENBANK ID: NM_001662
DEFINITION HOMO SAPIENS ADP-RIBOSYLATION FACTOR 5 (ARF5), MRNA.
VERSION NM_001662.2 GI:6995999
CDS 37..579
/CODON_START=1

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   1 CCGCGTCGGT GCCCGCGCCC CTCCCCGGGC CCCGCCATGG GCCTCACCGT GTCCGCGCTC
  61 TTTTCGCGGA TCTTCGGGAA GAAGCAGATG CGGATTCTCA TGGTTGGCTT GGATGCGGCT
 121 GGCAAGACCA CAATCCTGTA CAAACTGAAG TTGGGGGAGA TTGTCACCAC CATCCCAACC
 181 ATAGGCTTCA ATGTAGAAAC AGTGGAATAT AAGAACATCT GTTTCACAGT CTGGGACGTG
 241 GGAGGCCAGG ACAAGATTCG GCCTCTGTGG CGGCACTACT TCCAGAACAC TCAGGGCCTC
 301 ATCTTTGTGG TGGACAGTAA TGACCGGGAG CGGGTCCAAG AATCTGCTGA TGAACTCCAG
 361 AAGATGCTGC AGGAGGACGA GCTGCGGGAT GCAGTGCTGC TGGTATTTGC CAACAAGCAG
 421 GACATGCCCA ACGCCATGCC CGTGAGCGAG CTGACTGACA AGCTGGGGCT ACAGCACTTA
 481 CGCAGCCGCA CGTGGTATGT CCAGGCCACC TGTGCCACCC AAGGCACAGG TCTGTACGAT
 541 GGTCTGGACT GGCTGTCCCA CGAGCTGTCA AAGCGCTAAC CAGCCAGGGG CAGGCCCCTG
 601 ATGCCCGGAA GCTCCTGCGT GCATCCCCGG GATGACCAGA CTCCCGGACT CCTCAGGCAG
 661 TGCCCTTTCC TCCCACTTTT CCTCCCCCAT AGCCACAGGC CTCTGCTCCT GCTCCTGCCT
 721 GCATGTTCTC TCTGTTGTTG GAGCCTGGAG CCTTGCTCTC TGGGCACAGA GGGGTCCACT
 781 CTCCTGCCTG CTGGGACCTA TGGAAGGGGC TTCCTGGCCA AGGCCCCCTC TTCCAGAGGA
 841 GGAGCAGGGA TCTGGGTTTC CTTTTTTTTT TCTGTTTTGG GTGTACTCTA GGGGCCAGGT
 901 TGGGAGGGGG AAGGTGAGGG CTTCGGGTGG TGCTATAATG TGGCACTGGA TCTTGAGTAA
 961 TAAATTTGCT GTGGTTTG
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GENBANK ID: XM_048886.3
DEFINITION HOMO SAPIENS MICROSOMAL GLUTATHIONE S-TRANSFERASE 1 (MGST1), MRNA.
VERSION XM_048886.3 GI:18580621
CDS 89..556
/CODON_START=1

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   1 AGTCCCTGCA TTGCGCGCGA CCCGGCGGCG GGACAGGCTT GCTGCTTCCT CCTCCTCGGC
  61 CTCACCATTC CAGACCAAAA TTGAAAAAAT GGTTGACCTC ACCCAGGTAA TGGATGATGA
 121 AGTATTCATG GCTTTTGCAT CCTATGCAAC AATTATTCTT TCAAAAATGA TGCTTATGAG
 181 TACTGCAACT GCATTCTATA GATTGACAAG AAAGGTTTTT GCCAATCCAG AAGACTGTGT
 241 AGCATTTGGC AAAGGAGAAA ATGCCAAGAA GTATCTTCGA ACAGATGACA GAGTAGAACG
 301 TGTACGCAGA GCCCACCTGA ATGACCTTGA AAATATTATT CCATTTCTTG GAATTGGCCT
 361 CCTGTATTCC TTGAGTGGTC CCGACCCCTC TACAGCCATC CTGCACTTCA GACTATTTGT
 421 CGGAGCACGG ATCTACCACA CCATTGCATA TTTGACACCC CTTCCCCAGC CAAATAGAGC
 481 TTTGAGTTTT TTTGTTGGAT ATGGAGTTAC TCTTTCCATG GCTTACAGGT TGCTGAAAAG
 541 TAAATTGTAC CTGTAAAGAA AATCATACAA CTCAGCATCC AGTTGGCTTT TTAAGAATTC
 601 TGTACTTCCA ATTTATAATG AATACTTTCT TAGATTTTAG GTAGGAGGGG AGCAGAGGAA
 661 TTATGAACTG GGGTAAACCC ATTTTGAATA TTAGCATTGC CAATATCCTG TATTCTTGTT
 721 TTACATTTGG ATTAGAAATT TAACATAGTA ATTCTTAAGT CTTTTGTCTG ATTTTTAAAG
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       781 TACTTTCTTA TAAATTTGGA TCATGTTATG ATTTGTAACA TTCACACAAC ACCTCACTTT
       841 TGAATCTATA AAAGAATTGC ACGTATGAGA AACCTATATT TCAATACTGC TGAAACAGAC
       901 ATGAAATAAA GAATTTAAAG AATG

GENBANK ID:  X02162
DEFINITION  HUMAN MRNA FOR APOLIPOPROTEIN AI (APO AI)=.
VERSION     X02162.1  GI:28771
CDS             87..890
/CODON_START=1
         1 GAATTCAAAA AAAAAAGAAA AAAAAAAAAA AAAAAAAAAA AAAAAAAGAG AGACTGCGAG
        61 AAGGAGGTCC CCCACGGCCC TTCAGGATGA AAGCTGCGGT GCTGACCTTG GCCGTGCTCT
       121 TCCTGACGGG GAGCCAGGCT CGGCATTTCT GGCAGCAAGA TGAACCCCCC CAGAGCCCCT
       181 GGGATCGAGT GAAGGACCTG GCCACTGTGT ACGTGGATGT GCTCAAAGAC AGCGGCAGAG
       241 ACTATGTGTC CCAGTTTGAA GGCTCCGCCT TGGGAAAACA GCTAAACCTA AAGCTCCTTG
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       421 AGGATCTGGA GGAGGTGAAG GCCAAGGTGC AGCCCTACCT GGACGACTTC CAGAAGAAGT
       481 GGCAGGAGGA GATGGAGCTC TACCGCCAGA AGGTGGAGCC GCTGCGCGCA GAGCTCCAAG
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       841 GCTTCCTGAG CGCTCTCGAG GAGTACACTA AGAAGCTCAA CACCCAGTGA GGCGCCCGCC
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GENBANK ID:  XM_007441.1
DEFINITION  HOMO SAPIENS PRESENILIN 1 (ALZHEIMER DISEASE 3) (PSEN1), MRNA.
VERSION     XM_007441.1  GI:11435041
CDS             249..1652
/CODON_START=1

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       121 CTGGGAGCCT GCAAGTGACA ACAGCCTTTG CGGTCCTTAG ACAGCTTGGC CTGGAGGAGA
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       241 TTGCTCCAAT GACAGAGTTA CCTGCACCGT TGTCCTACTT CCAGAATGCA CAGATGTCTG
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       421 ACTCCCGGCA GGTGGTGGAG CAAGATGAGG AAGAAGATGA GGAGCTGACA TTGAAATATG
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2281 TGCCTTTGGC AATTCTTCTT CTCAAGCACT GACACTCATT ACCGTCTGTG ATTGCCATTT
2341 CTTCCCAAGG CCAGTCTGAA CCTGAGGTTG CTTTATCCTA AAAGTTTTAA CCTCAGGTTC
2401 CAAATTCAGT AAATTTTGGA AACAGTACAG CTATTTCTCA TCAATTCTCT ATCATGTTGA
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2581 CAGTAAGGCA GCTCTGTCGT GGTAGCAGAT GGTCCCATTA TTCTAGGGTC TTACTCTTTG
2641 TATGATGAAA AGAATGTGTT ATGAATCGGT GCTGTCAGCC CTGCTGTCAG ACCTTCTTCC
2701 ACAGCAAATG AGATGTATGC CCAAAGACGG TAGAATTAAA GAAGAGTAAA ATGGCTGTTG
2761 AAGC
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GENBANK ID:  XM_087242.1
DEFINITION  HOMO SAPIENS ARGINYL AMINOPEPTIDASE (AMINOPEPTIDASE B)-LIKE
1(RNPEPL1), MRNA.
VERSION     XM_087242.1  GI:18600482
CDS             700..1764
/CODON_START=1

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 121 TGGCTGGACC CAGAGCTGAC CTATGGCTGC GCCAAGCCCT TCGTCTTCAC CCAGGGCCAC
 181 TCCGTGTGCA ACCGCTCCTT CTTCCCGTGC TTCGACACAC CTGCCGTGAA GTGCACCTAC
 241 TCTGCCGTCG TCAAGGCGCC ATCGGGGGTG CAGGTGCTGA TGAGTGCCAC CCGGAGTGCA
 301 TACATGGAGG AAGAAGGCGT CTTCCACTTC CACATGGAGC ACCCCGTGCC CGCCTACCTC
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 421 GCCGAGCCAT GCCTCCTGCC CACGGCCACC AGCAAGCTGT CGGGCGCAGT GGAGCAGTGG
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GENBANK ID: S90469
DEFINITION CYTOCHROME P450 REDUCTASE [HUMAN, PLACENTA, MRNA PARTIAL, 2403 NT].
VERSION S90469.1 GI:247306
CDS 1..2031
/CODON_START=1

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2401 GTA
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GENBANK ID: NM_006254.1
DEFINITION HOMO SAPIENS PROTEIN KINASE C, DELTA (PRKCD), MRNA.
VERSION NM_006254.1 GI:5453969
CDS 59..2089
/CODON_START=1

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2101 AGAT
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DEFINITION  H.SAPIENS MRNA FOR MACROPAIN SUBUNIT DELTA.
VERSION     X61971.1  GI:296733
CDS             <1..543
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 421 CGGGATGGCT CCAGTGGAGG AGTGATCCGC CTGGCAGCCA TTGCAGAGTC AGGGGTAGAG
 481 CGGCAAGTAC TTTTGGGAGA CCAGATACCC AAATTCGCCG TTGCCACTTT ACCACCCGCC
 541 TGAATCCTGG GATTCTAGTA TGCAATAAGA GATGCCCTGT ACTGATGCAA AATTTAATAA
 601 AGTTTGTCAC AGAGAAAAAA AAAA
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GENBANK ID: AH005909.1

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GENBANK ID:  XM_088424.1
DEFINITION  HOMO SAPIENS RETINOID X RECEPTOR, ALPHA (RXRA), MRNA.
VERSION     XM_088424.1  GI:18571706
CDS             519..1016
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 361 CCACTTCCCA GTGGCTGCTT CCTGGGGACC CAGGGCACCC CGGCACCTTC AGGCACGCTC
 421 CTCAGCTGGT CACCTCCCGG CTTTGCCGTT CAGATGGGGC TCCTGAGGCT CAGGAGTGAA
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GENBANK ID: U41745.1
DEFINITION HUMAN PDGF ASSOCIATED PROTEIN MRNA, COMPLETE CDS.
VERSION U41745.1 GI:1136583
CDS 22..567
/CODON_START=1

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 361 GAGATTGAGA AGCAGAAGGC AAAAGAGCGT TACATGAAAA TGCACTTGGC CGGGAAGACA
 421 GAGCAAGCCA AGGCTGACCT GGCCCGGCTG GCCATCATCC GGAAACAGCG GGAGGAGGCT
 481 GCCCGGAAGA AGGAAGAGGA AAGGAAAGCA AAAGACGATG CCACATTGTC AGGAAAACGA
 541 ATGCAGTCAC TCTCCCTGAA TAAGTAACTG CGACCCGTGG GAGGAGATGC CGGGGACCTG
 601 GGCCGCGCTG CCAGGACCTC TGCTGTGTCT CGCCCACCCT GTGCCCTGGC GCCGCTGCAA
 661 CAGCCCCTCA TGGCCAGGAG CCCCCCATGC CTGGGCCTCC TCTTCATCTT GGCACAGAAA
 721 TTGTTTGGGG GATGGGGGGG GGACTGGGGG AGGGGTAGCT GCTATCTTTG AGACAGAAAG
 781 ATGCAGGACA GCATTTCATA TGTAACCATT TGAATGTTTT TGCTGTTTTT AGAATTC
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GENBANK ID: AH002617.1

GENBANK ID: XM_034862.1
DEFINITION HOMO SAPIENS INTERFERON REGULATORY FACTOR 1 (IRF1), MRNA.
VERSION XM_034862.1 GI:14726087
CDS 197..1174
/CODON_START=1

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   1 CGAGCCCCGC CGAACCGAGG CCACCCGGAG CCGTGCCCAG TCCACGCCGG CCGTGCCCGG
  61 CGGCCTTAAG AACCCGGCAA CCTCTGCCTT CTTCCCTCTT CCACTCGGAG TCGCGCTCCG
 121 CGCGCCCTCA CTGCAGCCCC TGCGTCGCCG GGACCCTCGC GCGCGACCGC CGAATCGCTC
 181 CTGCAGCAGA GCCAACATGC CCATCACTCG GATGCGCATG AGACCCTGGC TAGAGATGCA
 241 GATTAATTCC AACCAAATCC CGGGGCTCAT CTGGATTAAT AAAGAGGAGA TGATCTTCCA
 301 GATCCCATGG AAGCATGCTG CCAAGCATGG CTGGGACATC AACAAGGATG CCTGTTTGTT
 361 CCGGAGCTGG GCCATTCACA CAGGCCGATA CAAAGCAGGG GAAAAGGAGC CAGATCCCAA
 421 GACGTGGAAG GCCAACTTTC GCTGTGCCAT GAACTCCCTG CCAGATATCG AGGAGGTGAA
 481 AGACCAGAGC AGGAACAAGG GCAGCTCAGC TGTGCGAGTG TACCGGATGC TTCCACCTCT
 541 CACCAAGAAC CAGAGAAAAG AAAGAAAGTC GAAGTCCAGC CGAGATGCTA AGAGCAAGGC
 601 CAAGAGGAAG TCATGTGGGG ATTCCAGCCC TGATACCTTC TCTGATGGAC TCAGCAGCTC
 661 CACTCTGCCT GATGACCACA GCAGCTACAC AGTTCCAGGC TACATGCAGG ACTTGGAGGT
 721 GGAGCAGGCC CTGACTCCAG CACTGTCGCC ATGTGCTGTC AGCAGCACTC TCCCCGACTG
 781 GCACATCCCA GTGGAAGTTG TGCCGGACAG CACCAGTGAT CTGTACAACT TCCAGGTGTC
 841 ACCCATGCCC TCCACCTCTG AAGCTACAAC AGATGAGGAT GAGGAAGGGA AATTACCTGA
 901 GGACATCATG AAGCTCTTGG AGCAGTCGGA GTGGCAGCCA ACAAACGTGG ATGGGAAGGG
 961 GTACCTACTC AATGAACCTG GAGTCCAGCC CACCTCTGTC TATGGAGACT TTAGCTGTAA
1021 GGAGGAGCCA GAAATTGACA GCCCAGGGGG GGATATTGGG CTGAGTCTAC AGCGTGTCTT
1081 CACAGATCTG AAGAACATGG ATGCCACCTG GCTGGACAGC CTGCTGACCC CAGTCCGGTT
1141 GCCCTCCATC CAGGCCATTC CCTGTGCACC GTAGCAGGGC CCCTGGGCCC CTCTTATTCC
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1201 TCTAGGCAAG CAGGACCTGG CATCATGGTG GATATGGTGC AGAGAAGCTG GACTTCTGTG
1261 GGCCCCTCAA CAGCCAAGTG TGACCCCACT GCCAAGTGGG GATGGGGCCT CCCTCCTTGG
1321 GTCATTGACC TCTCAGGGCC TGGCAGGCCA GTGTCTGGGT TTTTCTTGTG GTGTAAAGCT
1381 GGCCCTGCCT CCTGGGAAGA TGAGGTTCTG AGACCAGTGT ATCAGGTCAG GGACTTGGAC
1441 AGGAGTCAGT GTCTGGCTTT TTCCTCTGAG CCCAGCTGCC TGGAGAGGGT CTCGCTGTCA
1501 CTGGCTGGCT CCTAGGGGAA CAGACCAGTG ACCCCAGAAA AGCATAACAC CAATCCCAGG
1561 GCTGGCTCTG CACTAAGAGA AAATTGCACT AAATGAATCT CGTTCCCAAA GAACTACCCC
1621 CTTTTCAGCT GAGCCCTGGG GACTGTTCCA AAGCCAGTGA AATGTGAAGG AAAGTGGGGT
1681 CCTTCGGGGC GATGCTCCCT CAGCCTCAGA GGAGCTCTAC CCTGCTCCCT GCTTTGGCTG
1741 AGGGGCTTGG GAAAAAAACT TGGCACTTTT TCGTGTGGAT CTTGCCACAT TTCTGATCAG
1801 AGGTGTACAC TAACATTTCC CCCGAGCTCT TGGCCTTTGC ATTTATTTAT ACAGTGCCTT
1861 GCTCGGCGCC CACCACCCCC TCAAGCCCCA GCAGCCCTCA ACAGGCCCAG GGAGGGAAGT
1921 GTGAGCGCCT TGGTATGACT TAAAATTGGA AATGTCATCT AACCATTAAG TCATGTGTGA
1981 ACACATAGGA CGTGTGTAAA TATGTACATT TGTCTTTTTA TAAAAAGTAA ATTGTT
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GENBANK ID: AJ310549.1

DEFINITION HOMO SAPIENS MRNA FOR CLP-36 PROTEIN.
VERSION AJ310549.1 GI:13160404
CDS 1..990
/CODON_START=1

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   1 ATGACCACCC AGCAGATAGA CCTCCAGGGC CCGGGGCCGT GGGGCTTCCG CCTCGTGGGC
  61 GGCAAGGACT TCGAGCAGCC TCTCGCCATT TCCCGGGTCA CTCCTGGAAG CAAGGCGGCT
 121 CTAGCTAATT TATGTATTGG AGATGTAATC ACAGCCATTG ATGGGGAAAA TACTAGCAAT
 181 ATGACACACT TGGAAGCTCA GAACAGAATC AAAGGCTGCA CAGACAACTT GACTCTCACT
 241 GTAGCCAGAT CTGAACATAA AGTCTGGTCT CCTCTGGTGA CGGAGGAAGG GAAGCGTCAT
 301 CCATACAAGA TGAATTTAGC CTCTGAACCC CAGGAGGTCC TGCACATAGG AAGCGCCCAC
 361 AACCGAAGTG CCATGCCCTT TACCGCCTCG CCTGCCTCCA GCACTACTGC CAGGGTCATC
 421 ACAAACCAGT ACAACAACCC AGCTGGCCTC TACTCTTCTG AAAATATCTC CAACTTCAAC
 481 AATGCCCTGG AGTCAAAGAC TGCTGCCAGC GGGGTGGAGG CGAACAGCAG ACCCTTAGAC
 541 CATGCTCAGC CTCCAAGCAG CCTTGTCATC GACAAAGAAT CTGAAGTTTA CAAGATGCTT
 601 CAGGAGAAAC AGGAGTTGAA TGAGCCCCCG AAACAGTCCA CGTCTTTCTT GGTTTTGCAG
 661 GAAATCCTGG AGTCTGAAGA AAAAGGGGAT CCCAACAAGC CCTCAGGATT CAGAAGTGTT
 721 AAAGCTCCTG TCACTAAAGT GGCTGCGTCG ATTGGAAATG CTCAGAAGTT GCCTATGTGT
 781 GACAAATGTG GCACTGGGAT TGTTGGTGTG TTTGTGAAGC TGCGGGACCG TCACCGCCAC
 841 CCTGAGTGTT ATGTGTGCAC TGACTGTGGC ACCAACCTGA AACAGAAGGG CCATTTCTTT
 901 GTGGAGGATC AAATCTACTG TGAGAAGCAT GCCCGGGAGC GAGTCACACC ACCTGAGGGT
 961 TATGAAGTGG TCACTGTGTT CCCCAAGTGA GCCAGCAGAT CTGACCACTG TTCTCCAGCA
1021 GGCCTCTGCT GCAGCTTTTT CTCTCAGTGT TCTGGCCCTC TCCTCTCTTG AAAGTTCTCT
1081 GCTTACTTTG GTT
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GENBANK ID: XM_016642.3
DEFINITION HOMO SAPIENS ADENYLATE KINASE 3 (AK3), MRNA.
VERSION XM_016642.3 GI:16163712
CDS 145..816
/CODON_START=1

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   1 CCTTCCCCCT GTAGGGCCGG CCGGCGAGTC CCAGTGAGAG CGGAGGGTGC CAGAGGTAGG
  61 GGGCCGAGAA ACAAAGTTCC CGGGGCTCCC TCCGGGGCCG CGGTCGGGGC TGCGCGTTTG
 121 ACCGCCCCCC TCCTCGCGAA GGCAATGGCT TCCAAACTCC TGCGCGCGGT CATCCTCGGG
 181 CCGCCCGGCT CGGGCAAGGG CACCGTGTGC CAGAGGATCG CCCAGAACTT TGGTCTCCAG
 241 CATCTCTCCA GCGGCCACTT CTTGCGGGAG AACATCAAGG CCAGCACCGA AGTTGGTGAG
 301 GTGGCAAAGC AGTATATAGA GAAAAGTCTT TTGGTTCCAG ACCATGTGAT CACACGCCTA
 361 ATGATGTCCG AGTTGGAGAA TAGGCGTGGC CAGCACTGGC TCCTTGATGG TTTTCCTAGG
 421 ACATTAGGAC AAGCCGAGGC CCTGGACAAA ATCTGTGAAG TGGATCTAGT GATCAGTTTG
 481 AATATTCCAT TTGAAACACT TAAAGATCGT CTCAGCCGCC GTTGGATTCA CCCTCCTAGC
 541 GGAAGGGTAT ATAACCTGGA CTTCAATCCA CCTCATGTAC ATGGTATTGA TGACGTCACT
 601 GGTGAACCAT TAGTCCAGCA GGAGGATGAT AAACCCGAAG CAGTTGCTGC CAGGCTAAGA
 661 CAGTACAAAG ACGCGGCAAA GCCAGTCATT GAATTATACA AGAGCCGAGG AGTGCTCCAC
 721 CAATTTTCCG GAACGGAGAC GAACAAAATC TGGCCCTACG TTTACACACT TTTCTCAAAC
 781 AAGATCACAC CTATTCAGTC CAAAGAAGCA TATTGACCCT GCCCAATGGA AGAACCAGGA
 841 AGATGTGGTC ATTCATTCAA TAGTGTGTGT AGTATTGGTG CTGTGTCCAA ATTAGAAGCT
 901 AGCTGAGGTA GCTTGCAGCA TCTTTTCTAG TTGAAATGGT GAACTGATAG GAAAACAAAT
 961 GAGTAGAAAG AGTTCATGAA GAGGCCCTCC TCTGCCTTTC AAAAGGGTGG TCACCTACAC
1021 ATGTTTAAGG TGTCTCTGCA CATGTCTCAA GCCCATCACA AGAAAGCAAG TACAGTGTGG
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1081 ATTTCAAATG GTGTGTAACT TCAGCTCCAG CTGGTTTTTG ACAGCTGTTG CTGTGGTAAT
1141 ATTTTTTACA TGTGATGGTG ATAGTCTCTG GTTCTCCCCA TCCCCACAAA GGCTGTTGAA
1201 CCACAGCACC AGGAAGCCTG AGAATGAATC CTGAGGGCTC TAGCCCAGGC TTTGTCCCAG
1261 GCTTTCTGGT GTGTGCCCTC CTGGTAACAG TGAAATTGAA GCTACTTACT CATAGTGGTT
1321 GTTTCTCTGG TCTTGAGTGA CTGTGTCCAC AGTTCATTTT TTTCCGGTAG GAATAACTCC
1381 TTTTCTACAT CCACACTCCA TAGAGTCTCT CCTTTTCAGA TATCCTGGGA TGAAAGAATT
1441 TGGCTTTTTT TTTTTTTTTT TTTTTGACAT CTGTTTTCAC TCTTAGGCTT TTAAACAATA
1501 GTTATTGCTC TTATCCCTCT CAGATTCTAA TAACTGAGAG TGATGGGGCT ATATTGAATC
1561 TCTGTATGCA CTGAGAACTG AGCTATGAAG AGGATCTTAT TAAACTGCTG GTCTGACTTT
1621 ATGGATTGAC ACTGTTCCTT TCTTTTATTG TG
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GENBANK ID: Z35307.1
DEFINITION H.SAPIENS MRNA FOR ENDOTHELIN-CONVERTING-ENZYME 1.
VERSION Z35307.1 GI:535181
CDS 38..2299
/CODON_START=1

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   1 CGCCCCCCCG GTGTCCGCCC TGCTGTCGGC GCTGGGGATG TCGACGTACA AGCGGGCCAC
  61 GCTGGACGAG GAGGACCTGG TGGACTCGCT CTCCGAGGGC GACGCATACC CCAACGGCCT
 121 GCAGGTGAAC TTCCACAGCC CCCGGAGTGG CCAGAGGTGC TGGGCTGCAC GGACCCAGGT
 181 GGAGAAGCGG CTGGTGGTGT TGGTGGTACT TCTGGCGGCA GGACTGGTGG CCTGCTTGGC
 241 AGCACTGGGC ATCCAGTACC AGACAAGATC CCCCTCTGTG TGCCTGAGCG AAGCTTGTGT
 301 CTCAGTGACC AGCTCCATCT TGAGCTCCAT GGACCCCACA GTGGACCCCT GCCATGACTT
 361 CTTCAGCTAC GCCTGTGGGG GCTGGATCAA GGCCAACCCA GTCCCTGATG GCCACTCACG
 421 CTGGGGGACC TTCAGCAACC TCTGGGAACA CAACCAAGCA ATCATCAAGC ACCTCCTCGA
 481 AAACTCCACG GCCAGCGTGA GCGAGGCAGA GAGAAAGGCG CAAGTATACT ACCGTGCGTG
 541 CATGAACGAG ACCAGGATCG AGGAGCTCAG GGCCAAACCT CTAATGGAGT TGATTGAGAG
 601 GCTCGGGGGC TGGAACATCA CAGGTCCCTG GGCCAAGGAC AACTTCCAGG ACACCCTGCA
 661 GGTGGTCACC GCCCACTACC GCACCTCACC CTTCTTCTCT GTCTATGTCA GTGCCGATTC
 721 CAAGAACTCC AACAGCAACG TGATCCAGGT GGACCAGTCT GGCCTGGGCT TGCCCTCGAG
 781 AGACTATTAC CTGAACAAAA CTGAAAACGA GAAGGTGCTG ACCGGATATC TGAACTACAT
 841 GGTCCAGCTG GGGAAGCTGC TGGGCGGCGG GGACGAGGAG GCCATCCGGC CCCAGATGCA
 901 GCAGATCTTG GACTTTGAGA CGGCACTGGC CAACATCACC ATCCCACAGG AGAAGCGCCG
 961 TGATGAGGAG CTCATCTACC ACAAAGTGAC GGCAGCCGAG CTGCAGACCT TGGCACCCGC
1021 CATCAACTGG TTGCCTTTTC TCAACACCAT CTTCTACCCC GTGGAGATCA ATGAATCCGA
1081 GCCTATTGTG GTCTATGACA AGGAATACCT TGAGCAGATC TCCACTCTCA TCAACACCAC
1141 CGACAGATGC CTGCTCAACA ACTACATGAT CTGGAACCTG GTGCGGAAAA CAAGCTCCTT
1201 CCTTGACCAG CGCTTTCAGG ACGCCGATGA GAAGTTCATG GAAGTCATGT ACGGGACCAA
1261 GAAGACCTGT CTTCCTCGCT GGAAGTTTTG CGTGAGTGAC ACAGAAAACA ACCTGGGCTT
1321 TGCGTTGGGC CCCATGTTTG TCAAAGCAAC CTTCGCCGAG GACAGCAAGA GCATAGCCAC
1381 CGAGATCATC CTGGAGATTA AGAAGGCATT TGAGGAAAGC CTGAGCACCC TGAAGTGGAT
1441 GGATGAGGAA ACCCGAAAAT CAGCCAAGGA AAAGGCCGAT GCCATCTACA ACATGATAGG
1501 ATACCCCAAC TTCATCATGG ATCCCAAGGA GCTGGACAAA GTGTTTAATG ACTACACTGC
1561 AGTTCCAGAC CTCTACTTTG AAAATGCCAT GCGGTTTTTC AACTTCTCAT GGAGGGTCAC
1621 TGCCGATCAG CTCAGGAAAG CCCCCAACAG AGATCAGTGG AGCATGACCC CGCCCATGGT
1681 GAACGCCTAC TACTCGCCCA CCAAGAATGA GATTGTGTTT CCGGCCGGGA TCCTGCAGGC
1741 ACCATTCTAC ACACGCTCCT CACCCAAGGC CTTAAACTTT GGTGGCATAG GTGTCGTCGT
1801 GGGCCATGAG CTGACTCATG CTTTTGATGA TCAAGGACGG GAGTATGACA AGGACGGGAA
1861 CCTCCGGCCA TGGTGGAAGA ACTCATCCGT GGAGGCCTTC AAGCGTCAGA CCGAGTGCAT
1921 GGTAGAGCAG TACAGCAACT ACAGCGTGAA CGGGGAGCCG GTGAACGGGC GGCACACCCT
1981 GGGGGAGAAC ATCGCCGACA ACGGGGGTCT CAAGGCGGCC TATCGGGCTT ACCAGAACTG
2041 GGTGAAGAAG AACGGGGCTG AGCACTCGCT CCCCACCCTG GGCCTCACCA ATAACCAGCT
2101 CTTCTTCCTG GGCTTTGCAC AGGTCTGGTG CTCCGTCCGC ACACCTGAGA GCTCCCACGA
2161 AGGCCTCATC ACCGATCCCC ACAGCCCCTC TCGCTTCCGG GTCATCGGCT CCCTCTCCAA
2221 TTCCAAGGAG TTCTCAGAAC ACTTCCGCTG CCCACCTGGC TCACCCATGA ACCCGCCTCA
2281 CAAGTGCGAA GTCTGGTAAG GACGAAGCGG AGAGAGCCAA GACGGAGGAG GGGAAGGGGC
2341 TGAGGACGAG ACCCCCATCC AGCCTCCAGG GCATTGCTCA GCCCGCTTGG CCACCCGGGG
2401 CCCTGCTTCC TCACACTGGC GGGTTTTCAG CCGGAACCGA GCCCATGGTG TTGGCTCTCA
2461 ACGTGACCCG CAGTCTGATC CCCTGTGAAG AGCCGGACAT CCCAGGCACA CGTGTGCGCC
2521 ACCTTCAGCA GGCATTCGGG TGCTGGGCTG GTGGCTCATC AGGCCTGGGC CCCACACTGA
2581 CAAGCGCCAG ATACGCCACA AATACCACTG TGTCAAATGC TTTCAAGATA TATTTTTGGG
2641 GAAACTATTT TTTAAACACT GTGGAATACA CTGGAAATCT TCAGGGAAAA ACACATTTAA
2701 ACACTTTTTT TTTTAAGCCC
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GENBANK ID: J02683
DEFINITION HUMAN ADP/ATP CARRIER PROTEIN MRNA, COMPLETE CDS.

VERSION J02683.1 GI:179246
CDS 70..966
/CODON_START=1

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   1 CCGCAGCGCC GTAGTCAAAC CGAACCCGGC CCAGTCCCGT CCTGCAGCAG TCTGCCTCCT
  61 TCTTTCAACA TGACAGATGC CGCATTGTCC TTCGCCAAGG ACTTCCTGGC AGGTGGAGTG
 121 GCCGCAGCCA TCTCCAAGAC GGCGGTAGCG CCCATCGAGC GGGTCAAGCT GCTGCTGCAG
 181 GTGCAGCATG CCAGCAAGCA GATCACTGCA GATAAGCAAT ACAAAGGCAT TATAGACTGC
 241 GTGGTCCGTA TTCCCAAGGA GCAGGAAGTT CTGTCCTTCT GGCGCGGTAA CCTGGCCAAT
 301 GTCATCAGAT ACTTCCCCAC CCAGGCTCTT AACTTCGCCT TCAAAGATAA ATACAAGCAG
 361 ATCTTCCTGG GTGGTGTGGA CAAGAGAACC CAGTTTTGGC GCTACTTTGC AGGGAATCTG
 421 GCATCGGGTG GTGCCGCAGG GGCCACATCC CTGTGTTTTG TGTACCCTCT TGATTTTGCC
 481 CGTACCCGTC TAGCAGCTGA TGTGGGTAAA GCTGGAGCTG AAAGGGAATT CCGAGGCCTC
 541 GGTGACTGCC TGGTTAAGAT CTACAAATCT GATGGGATTA AGGGCCTGTA CCAAGGCTTT
 601 AACGTGTCTG TGCAGGGTAT TATCATCTAC CGAGCCGCCT ACTTCGGTAT CTATGACACT
 661 GCAAAGGGAA TGCTTCCGGA TCCCAAGAAC ACTCACATCG TCATCAGCTG GATGATCGCA
 721 CAGACTGTCA CTGCTGTTGC CGGGTTGACT TCCTATCCAT TTGACACCGT TCGCCGCCGC
 781 ATGATGATGC AGTCAGGGCG CAAAGGAACT GACATCATGT ACACAGGCAC GCTTGACTGC
 841 TGGCGGAAGA TTGCTCGTGA TGAAGGAGGC AAAGCTTTTT TCAAGGGTGC ATGGTCCAAT
 901 GTTCTCAGAG GCATGGGTGG TGCTTTTGTG CTTGTCTTGT ATGATGAAAT CAAGAAGTAC
 961 ACATAAGTTA TTTCCTAGGA TTTTTCCCCC TGTGAACAGG CATGTTGTAT TCTATAACAC
1021 AATCTTGAGC ATTCTTGACA GACTCCTGGC TGTCAGTTTC TCAGTGGCAA CTACTTTACT
1081 GGTTGAAAAT GGGAAGCAAT AATATTCATC TGACCAGTTT TCTCTTAAAG CCATTTCCAT
1141 GCATGATGAT GATGGGACTC AATTGTATTT TTTATTTCAG TCACTCCTGA CTAAATAACA
1201 ATTTGGAGAA ATAAAAATAG TCTAAAAT
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GENBANK ID: M22760.1
DEFINITION HOMO SAPIENS NUCLEAR-ENCODED MITOCHONDRIAL CYTOCHROME C OXIDASE VA SUBUNIT MRNA, COMPLETE CDS.
VERSION M22760.1 GI:695359
20..472
/CODON_START=1

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   1 GGGCGCCGCC ATCGCCGTCA TGCTGGGCGC CGCTCTCCGC CGCTGCGCTG TGGCCGCAAC
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 121 TATCCAGTCA GTTCGCTGCT ATTCCCATGG GTCACAGGAG ACAGATGAGG AGTTTGATGC
 181 TCGCTGGGTA ACATACTTCA ACAAGCCAGA TATAGATGCC TGGGAATTGC GTAAAGGGAT
 241 AAACACACTT GTTACCTATG ATATGGTTCC AGAGCCCAAA ATCATTGATG CTGCTTTGCG
 301 GGCATGCAGA CGGTTAAATG ATTTTGCTAG TCTAGTTCGA ATCCTAGAGG TTGTTAAGGA
 361 CAAAGCAGGA CCTCATAAGG AAATCTACCC CTATGTCATC CAGGAACTTA GACCAACTTT
 421 AAATGAACTG GGAATCTCCA CTCCGGAGGA ACTGGGCCTT GACAAAGTGT AAACCGCATG
 481 GATGGGCTTC CCCAAGGATT TATTGACATT GCTACTTGAG TGTGAACAGT TACCTGGAAA
 541 TACTGATGAT AACATATTAC CTTATTTTGA ACAAGTTTCC CTTTATTGAG TACCAAGCCA
 601 TGTAATGGTA ACTTGGACTT TAATAAAAGG GAAATGAGTT TGAACTG
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GENBANK ID: M18079
DNA LINEAR
DEFINITION HUMAN, INTESTINAL FATTY ACID BINDING PROTEIN GENE, COMPLETE CDS,AND AN ALU REPETITIVE ELEMENT.
VERSION M18079.1 GI:182351

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   1 GTAATATCTT GGGCAAGCCC TAGAGCTTCT TTCCTGACCC TTAGTTAATA AGATGTTATC
  61 TGGTCACATT CAGTCACAAT AATAGACTCA TTTTAGTAAT AAACATCTTA AGACTAGTAA
 121 TTAAAACTCT TTACTTCACA CCAAGTTTCC TCCCCAAGCT TGGCCTGTTC CTGGCTGGCA
 181 GCCTGAAGTA GGGAAAGGAG AGATATGGTG ACCTTTTCTT TGTACCTTTC TAGCTACCCT
 241 CTATACCCTG ACCCCACATA CATAATTGAG CTGTGGCTTC TGACTCTACT GGGTTTGGGG
 301 ATGAGAGGCA GTGAGAGTAA AATGAAGGAG TGGTTTTAAT TAATGGCACA GCTAAAACTG
 361 GATTTTGTTC TCTCTGCACA TGGCAGATGT TTAAAGCTCA TTCTTTCTTT TATGCAAGTT
 421 TTTACACCAT CCAGCCTCAT TTGTACCTCT TGAATTTTTG CTCAGTGGCC TATCACCATT
 481 CAGGATCAAG ACAAAAATCA ATGAGCACTT ATTGTGTGTC ATGCACCCTA CAAAGTGCCA
 541 GGATATTTAT CCAAACTCCT GGCAATGCTA AACACAATGC AAAAAGACAT ATTAGAAAAC
 601 GAATCTTATT AACTTTAGCT TTTCAACTGT ATTTCATCAT AAAGTCTTAC TTTACAAGAT
 661 AATTGCTGTT GTGAAAAAGG GAAAGGTCAT GGTCTCATTT CCCAGATGTT ATTTGATATA
 721 TGCTATAAAT TATATTACCT CCAACATAGT CTGCACTTTG AACTTAGAAA AACAATCTTC
 781 AGACGGCATG CATTCTAATT CTTGAAATAA GTATGCCCAC AAACTGTAGT TTAAGACAGA
 841 ATAGGTATGC TTCTCATGTT TTAATTCAGT TGAATTTCAG AAGATCTCAG GAATGTACAG
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 901 AACGAGAATT AAGAATTAAT AAGAATAAGA ATTAATTAAT TGCTTGACAT AGAGTAGTTA
 961 GGTGATTTCC TGAACTTTAA GCTTCCACAT CACAGTATGA AGTTGGTTCA AGATAAGAAA
1021 TATAATAAAT TCTCGCCCAA GGACAGACCT GAATCTCTAG CTGCCTAGAG GCTGACTCAA
1081 CTGAAATCAT GGCGTTTGAC AGCACTTGGA AGGTAGACCG GAGTGAAAAC TATGACAAGT
1141 TCATGGAAAA AATGGGTAAA GACTTTATTT CTTTGTGGCT CATTCTTTGC TTTCTTACAA
1201 ACATTTTTCT TTCTAACTCC TAAATCTCTA GGAGATTACA GATAGCTTAC AGATAGCTCC
1261 TGATGTGGTA GAGAGGGATC CAGAAGATGT TCAGAGGAGG GAAACCATAT TTTCCCTTCT
1321 TACATTAGGA AGAATCCACT ATCTCACTAA TGGAAGAAAA GATTCTTTGA GTGCTGTTCT
1381 CTGAAACACA CCAAAAAGAT CCAGAAATGT TTCCTTCACT CTTTAACTGA AAAATGACTT
1441 TTTTTGTTGT TTACAGTAAG AAAATGGCAG CGTGTAATGA TAACTTCCAG ATCTGAAAAT
1501 GTTAAATTCT AGGAGATGGA AAAACAAAGA CCATATAAGA AAGTAATGGA AAAAGTTCTC
1561 TTAAAATTTA TAGCTCTGAA TAAGTTAGAT TTAATTCTGA TTTCTTCTAA CTTAAAAAAG
1621 TTTTGGAATA ATCTTGAGAA GCTGTGTAGT TTTCTCCAGG GCGTTTAATT TAACTGATTT
1681 ATAATTTGAT ACCAATACTC TGGCAGCCCA TATACTATAC AAGATAGGCA AACAAATTTG
1741 TGTCATTCCC CTAAAAGAAA AATCTGCATC AATTATAGCT TACAGTTTAG GAACTCTAAG
1801 TTTAAATTTA TAAAAGTTGT AGATTCTTAT AGTGATTTTG GCTTAATATT TGCTAATTTT
1861 CTCATTTTTG TGTCAGAAAG AAATGCCACA AGAAGCAAAT AGAACTATAA AGTTCAAAAT
1921 GTTAAAGCCA CTAAGAAAAA CAAAGGGGCA TTTAAGAAAA AAGAATACTG TATATGTGGA
1981 ATTAAAGATG TGCTTCCTTA TAAATATATG AATATACATT TTAATCCTTC ATTTAATATT
2041 TCTAGAATTT GATTTACTTA ACACTGAAAT GAACAGTTTG TTAATCTTAT TAAGGTTGCT
2101 CAGCTCTAAG ATTCTATAAT TCTGTACTCT ACTTAATTTT TCTCAAGTTA TGGAAAAACA
2161 ACTTTAATCA GTTCTCTTGA TCGGATTGAA CCTGAACTTC TATAGAAGCA ATCTGAATGT
2221 TCTTGTGCAA AGGCAATGCT ACCGAGTTTT CTTCCCACCC TCAAAATAAA CAAACAAAAC
2281 ATAACTTGGA AAAATAAACA CTTCCTATGG GATTTGACTT TATTTTCTCC ATTGTCTTAC
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2401 CAATTACACA AGAAGGAAAT AAATTCACAG TCAAAGAATC AAGCGCTTTT CGAAACATTG
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2521 GGGTAAGAAT TTTTTTTTTT ATGAGCAATG CATTCTTGAT TTTTCTACCC AATATTAAAA
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2821 AGTACAGCAA AAGAAGCCTT TAGAGTTAAT ATGTAACTTA ACTGTAACAT GTTGAAATAA
2881 TAAAAGAAAT GAATAGATGA ACAAATGAGT GAGTTACCAA ATGGAAAGAT TTGATGTATT
2941 GTAGGTCATT GGGAGTGTAC CTTTTCATGT TTAAGATAAC ACATTTTAGG AAGTCATCAT
3001 TTTCAACAAA TTTTTTAAAA ACTTTTTTTA GCCTCAACAT TTTTCTATTT AAATTACATG
3061 TTTGTAATGA CAATTTAACT ACTGAATGTT TTATCGTAAG TTATGTCTTT CCTTAATTAG
3121 TACCACAATC ACACAAATTA AAACAAGCAC AGGTTATTAA CATCTCCGTG AAACTAATTT
3181 TAACCATGAC TATATTTCTG GACACGTAAC ATGAAAGATT CAGAAAGAAG TGCTGCTCAT
3241 CTGCCTTAAA ATTCAGCGTA TGGAAATTAT TGAAGAGAAC AAGCATAATG GTTATCAACA
3301 CATACTCTGT AGCCCAATGG CCTAGGTTCA ATCCTCACTC TGTGACTTTA GGTGAATCAC
3361 TGTGCCATTT TACAGTCTCC TCTTCTGCAA AGTAGAGATA GTAGTATCAG TTTCATAGGG
3421 TCACCATGAA GATTAAATGA AAAAGTGTGT CTACAGAACT CAGAACAGTG CCTGACATGT
3481 GTAAGACCCT AATAAATGCC ATTATTATTA TTATTATTAT TATTATTATT ATTATTATTA
3541 TGTAGGGGAC CTGGAGCCTT GAGGGAAATA AACTTATTGG AAAATTCAAA CGGACAGACA
3601 ATGGAAACGA ACTGAATACT GTCCGAGAAA TTATAGGTGA TGAACTAGTC CAGGTGAGTT
3661 GTCAAATTTA TAGCTATTTT CAAAAGGCAA AAATTACTAC AAAACAATAA TTTTTGTCAC
3721 TGCTGAGCCA GATCTTCAGT AAACTGACTA CTTCTTTTCT CATAAATCTT ACTGATTTTA
3781 AAAATATTGT ATAGCTATTT TCTGATGCCT ATTTACTAAA GACAACTTAT ATATGTCAAA
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GENBANK ID: X16277
DNA     LINEAR
DEFINITION  HUMAN GENE FOR ORNITHINE DECARBOXYLASE ODC (EC 4.1.1.17).
VERSION     X16277.1  GI:35137
MRNA            JOIN(795..1001,3858..3967,4073..4191,4475..4648,
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VERSION X57522.1 GI:36060
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GENBANK ID: D00017.1
DEFINITION HOMO SAPIENS MRNA FOR LIPOCORTIN II, COMPLETE CDS.
VERSION D00017.1 GI:219909
CDS 50..1069
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 961 GTCTGAATTC AAGAGAAAGT ACGGCAAGTC CCTGTACTAT TATATCCAGC AAGACACTAA
1021 GGGCGACTAC CAGAAAGCGC TGCTGTACCT GTGTGGTGGA GATGACTGAA GCCCGACACG
1081 GCCTGAGCGT CCAGAAATGG TGCTCACCAT GCTTCCAGCT AACAGGTCTA GAAAACCAGC
1141 TTGCGAATAA CAGTCCCCGT GGCCATCCCT GTGAGGGTGA CGTTAGCATT ACCCCCAACC
1201 TCATTTTAGT TGCCTAAGCA TTGCCTGGCC TTCCTGTCTA GTCTCTCCTG TAAGCCAAAG
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1321 GTACTGTGTC ATAAACAGAT GAATAAACTG AATTTGTACT TT
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GENBANK ID: M10277.1
DNA LINEAR
DEFINITION HUMAN CYTOPLASMIC BETA-ACTIN GENE, COMPLETE CDS.
VERSION M10277.1 GI:177967

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   1 GCCCAGCACC CCAAGGCGGC CAACGCCAAA ACTCTCCCTC CTCCTCTTCC TCAATCTCGC
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 121 GCGGCGAAGC CGGTGAGTGA GCGGCGCGGG GCCAATCAGC GTGCGCCGTT CCGAAAGTTG
 181 CCTTTTATGG CTCGAGCGGC CGCGGCGGCG CCCTATAAAA CCCAGCGGCG CGACGCGCCA
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 421 GCCGTGGGGG GCGCGGGAGA AGCCCCTGGG CCTCCGGAGA TGGGGGACAC CCCACGCCAG
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 781 CGAGCCGCTG GCGCCCGAGG GTGTGGCCGC TGCGTGCGCG CGCGCGACCC GGTCGCTGTT
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GENBANK ID:  XM_042788.1
DEFINITION  HOMO SAPIENS ALDOLASE B, FRUCTOSE-BISPHOSPHATE (ALDOB), MRNA.
VERSION     XM_042788.1  GI:14738248
CDS             126..1220
/CODON_START=1
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 121 TCACCATGGC CCACCGATTT CCAGCCCTCA CCCAGGAGCA GAAGAAGGAG CTCTCAGAAA
 181 TTGCCCAGAG CATTGTTGCC AATGGAAAGG GGATCCTGGC TGCAGATGAA TCTGTAGGTA
 241 CCATGGGGAA CCGCCTGCAG AGGATCAAGG TGGAAAACAC TGAAGAGAAC CGCCGGCAGT
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       301 TCCGAGAAAT CCTCTTCTCT GTGGACAGTT CCATCAACCA GAGCATCGGG GGTGTGATCC
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       421 AGGAAAAGGG GATCGTGGTG GGAATCAAGT TAGACCAAGG AGGTGCTCCT CTTGCAGGAA
       481 CAAACAAAGA AACCACCATT CAAGGGCTTG ATGGCCTCTC AGAGCGCTGT GCTCAGTACA
       541 AGAAAGATGG TGTTGACTTT GGGAAGTGGC GTGCTGTGCT GAGGATTGCC GACCAGTGTC
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       661 AGCAGAATGG ACTGGTACCT ATTGTTGAAC CAGAGGTAAT TCCTGATGGA GACCATGACC
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GENBANK ID: NM_005317.2
DEFINITION HOMO SAPIENS GRANZYME M (LYMPHOCYTE MET-ASE 1) (GZMM), MRNA.
VERSION NM_005317.2 GI:7108347
CDS 46..819
/CODON_START=1

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GENBANK ID: XM_003595.2
DEFINITION HOMO SAPIENS GLUTAMYL AMINOPEPTIDASE (AMINOPEPTIDASE A)
(ENPEP),MRNA.
VERSION XM_003595.2 GI:13647140
CDS 1401..2957
/CODON_START=1

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       181 GTGGGACTTG CCGTGGGCTT GACCAGATCG TGTGACTCCA GCGGGGACGG CGGGCCGGGC
       241 ACTGCGCCAG CTCCTTCCCA CCTGCCTTCT TCCACGGCCA GCCCCTCAGG TCCTCCTGCC
       301 CAGGACCAGG ACATCTGCCC GGCCAGTGAG GATGAGAGCG GACAGTGGAA AAACTTTCGA
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2881 AAAACAATAT AGAGTGGCTA AAACAACATA GAAACACCAT CAGAGAATGG TTTTTTAATT
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GENBANK ID: U34683.1
DEFINITION  HUMAN GLUTATHIONE SYNTHETASE MRNA, COMPLETE CDS.
VERSION     U34683.1  GI:1236349
CDS             41..1465
/CODON_START=1
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GENBANK ID:  AF035429.1
DNA     LINEAR
DEFINITION  HOMO SAPIENS CYTOCHROME OXIDASE SUBUNIT I (COI) AND SUBUNIT II
(COII) PSEUDOGENES, COMPLETE SEQUENCE.
VERSION     AF035429.1  GI:2665724

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2041 ACAGACGAGG TCAACGATCC CTCCTTTACC ATCAAATCAA TTGGCCATCA ATGGTACTGA
2101 ACCTACGAAT ACACCGACTA CGGCGGACTA ATCTTCAACT CCTACATACT TCCCCCATTA
2161 TTCCTAGAAC CAGGCGACCT GCGACTCCTT GACGTTGACA ATCGAGTAGT ACTCCCGGTT
2221 GAAGCCCCCA TTCGTATAAT AATTACATCA CAAGACGTCT TACACTCATG AGCTGTCCCC
2281 ACATTAGGCT TAAAAACAGA TGCAATTCCC GGACGTCTAA ACCAAACCAC TTTCACTGCT
2341 ACACGACCAG GGGTATACTA CGGCCAATGC TCTGAAATCT GTGGAGCAAA CCAGTTTTAT
2401 GCCCATCGTC CTAGAATTAA TTCCCCTAAA AATCTTTGAA ATAGGGCCTG TATTTACCCT
2461 ATAGCACCCC CTCTACCCCC TCTAGAGCCC ACTGTAAAGC TAACTTAGCA TTAACCTTTT
2521 AAGTTAAAGA TTAAGAGAAC CAACACCTCT TTACAGTGAA ATGCCCCAAC TAAATACTA
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GENBANK ID:  NM_024409.1
DEFINITION  HOMO SAPIENS NATRIURETIC PEPTIDE PRECURSOR C (NPPC), MRNA.
VERSION     NM_024409.1  GI:13249345
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CDS             1..381
/CODON_START=1

        1 ATGCATCTCT CCCAGCTGCT GGCCTGCGCC CTGCTGCTCA CGCTGCTCTC CCTCCGGCCC
       61 TCCGAAGCCA AGCCCGGGGC GCCGCCGAAG GTCCCGCGAA CCCCGCCGGC AGAGGAGCTG
      121 GCCGAGCCGC AGGCTGCGGG CGGCGGTCAG AAGAAGGGCG ACAAGGCTCC CGGGGGCGGG
      181 GGCGCCAATC TCAAGGGCGA CCGGTCGCGA CTGCTCCGGG ACCTGCGCGT GGACACCAAG
      241 TCGCGGGCAG CGTGGGCTCG CCTTCTGCAA GAGCACCCCA ACGCGCGCAA ATACAAAGGA
      301 GCCAACAAGA AGGGCTTGTC CAAGGGCTGC TTCGGCCTCA AGCTGGACCG AATCGGCTCC
      361 ATGAGCGGCC TGGGATGTTA G

GENBANK ID:  M37763.1
DNA     LINEAR
DEFINITION  HUMAN NEUROTROPHIN-3 (NT-3) GENE, COMPLETE CDS.
VERSION     M37763.1  GI:189300
CDS             76..849
/CODON_START=1
GENE            76..849
MAT_PEPTIDE     130..846

        1 TAACACAGAC TCAGCTGCCA GAGCCTGCTC TTAACACCTG TGTTTCCTTT TCAGATCTTA
       61 CAGGTGAACA AGGTGATGTC CATCTTGTTT TATGTGATAT TTCTCGCTTA TCTCCGTGGC
      121 ATCCAAGGTA ACAACATGGA TCAAAGGAGT TTGCCAGAAG ACTCGCTCAA TTCCCTCATT
      181 ATTAAGCTGA TCCAGGCAGA TATTTTGAAA AACAAGCTCT CCAAGCAGAT GGTGGACGTT
      241 AAGGAAAATT ACCAGAGCAC CCTGCCCAAA GCTGAGGCTC CCCGAGAGCC GGAGCGGGGA
      301 GGGCCCGCCA AGTCAGCATT CCAGCCGGTG ATTGCAATGG ACACCGAACT GCTGCGACAA
      361 CAGAGACGCT ACAACTCACC GCGGGTCCTG CTGAGCGACA GCACCCCCTT GGAGCCCCCG
      421 CCCTTGTATC TCATGGAGGA TTACGTGGGC AGCCCCGTGG TGGCGAACAG AACATCACGG
      481 CGGAAACGGT ACGCGGAGCA TAAGAGTCAC CGAGGGGAGT ACTCGGTATG TGACAGTGAG
      541 AGTCTGTGGG TGACCGACAA GTCATCGGCC ATCGACATTC GGGGACACCA GGTCACGGTG
      601 CTGGGGGAGA TCAAAACGGG CAACTCTCCC GTCAAACAAT ATTTTTATGA AACGCGATGT
      661 AAGGAAGCCA GGCCGGTCAA AAACGGTTGC AGGGGTATTG ATGATAAACA CTGGAACTCT
      721 CAGTGCAAAA CATCCCAAAC CTACGTCCGA GCACTGACTT CAGAGAACAA TAAACTCGTG
      781 GGCTGGCGGT GGATACGGAT AGACACGTCC TGTGTGTGTG CCTTGTCGAG AAAAATCGGA
      841 AGAACATGAA TTGGCATCTC TCCCCATATA TAAATTATTA CTTTAAATTA TATGATATGC
      901 ATGTAGCATA TAAATGTTTA TATTGTTTTT ATATATTATA AGTTGACCTT TATTTATTAA
      961 ACTTCAGCAA CCCTACAGTA TATAAGCTTT TTTCTCAATA AAATCAGTGT GCTTGCCTTC

GENBANK ID:  NM_000932.1
DEFINITION  HOMO SAPIENS PHOSPHOLIPASE C, BETA 3
            (PHOSPHATIDYLINOSITOL-SPECIFIC) (PLCB3), MRNA.
VERSION     NM_000932.1  GI:11386138
CDS             1..3705

        1 ATGGCGGGCG CCCAGCCCGG CGTCCACGCG CTGCAGTTGG AGCCGCCCAC CGTGGTGGAG
       61 ACCCTGCGGC GCGGGAGTAA GTTCATCAAA TGGGACGAGG AGACCTCCAG TCGGAACCTG
      121 GTGACCCTGC GTGTGGACCC CAATGGCTTC TTCTTGTACT GGACGGGCCC CAACATGGAG
      181 GTGGACACAC TGGACATCAG TTCCATCAGG GACACACGGA CAGGCCGGTA CGCCCGCCTG
      241 CCCAAGGACC CCAAGATCCG GGAAGTTCTG GGCTTTGGGG GTCCCGATGC CCGGCTGGAG
      301 GAGAAGCTGA TGACGGTGGT GTCTGGGCCA GACCCGGTGA ACACAGTGTT CTTGAACTTC
      361 ATGGCCGTGC AGGATGACAC AGCCAAGGTC TGGTCTGAGG AGCTATTCAA GCTGGCTATG
      421 AACATCCTGG CTCAGAACGC CTCCCGGAAC ACCTTCCTGC GCAAAGCATA CACGAAGCTG
      481 AAGCTGCAGG TGAACCAGGA TGGTCGGATC CCCGTCAAGA ACATCCTGAA GATGTTCTCA
      541 GCAGACAAGA AGCGGGTGGA GACTGCGCTG GAATCCTGTG GCCTCAAATT CAACCGGAGT
      601 GAGTCCATCC GGCCTGATGA GTTTTCCTTG GAAATCTTTG AGCGGTTCCT GAACAAGCTG
      661 TGTCTGCGGC CGGACATTGA CAAGATCCTG CTGGAGATAG GCGCCAAGGG CAAGCCATAC
      721 CTGACGCTGG AGCAGCTCAT GGACTTCATC AACCAGAAGC AACGCGACCC GAGACTCAAC
      781 GAAGTGCTGT ACCCGCCCCT GCGGCCCTCC CAGGCCCGGC TGCTCATCGA AAAGTATGAG
      841 CCCAACCAGC AGTTTCTGGA GCGAGACCAG ATGTCCATGG AGGGCTTTAG CCGCTACCTG
      901 GGAGGCGAGG AGAATGGCAT CCTGCCCCTG GAAGCCCTGG ATCTGAGCAC GGACATGACC
      961 CAGCCACTGA GTGCCTACTT CATCAACTCC TCGCATAACA CCTATCTCAC TGCGGGGCAG
     1021 CTGGCTGGGA CCTCGTCGGT GGAGATGTAC CGCCAGGCAC TACTATGGGG CTGCCGCTGC
     1081 GTGGAGCTGG ACGTGTGGAA GGGACGGCCG CCTGAGGAGG AACCCTTCAT TACCCACGGC
     1141 TTCACCATGA CCACAGAGGT GCCTCTGCGC GACGTGCTGG AGGCCATTGC CGAGACTGCC
     1201 TTCAAGACCT CGCCCTACCC CGTCATCCTC TCCTTCGAGA ACCATGTGGA CTCGGCAAAG
     1261 CAACAGGCAA AGATGGCTGA GTACTGCCGC TCCATCTTTG GAGACGCGCT ACTCATCGAG
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1321 CCTCTGGACA AGTACCCGCT GGCCCCAGGC GTTCCCCTGC CCAGCCCCCA GGACCTGATG
1381 GGCCGTATCC TGGTGAAGAA CAAGAAGCGG CACCGACCCA GCGCAGGTGG CCCAGACAGC
1441 GCCGGGCGCA AGCGGCCCCT GGAGCAGAGC AATTCTGCCC TGAGCGAGAG CTCCGCGGCC
1501 ACCGAGCCCT CCTCCCCGCA GCTGGGGTCT CCCAGCTCTG ACAGCTGCCC AGGCCTGAGC
1561 AATGGGGAGG AGGTAGGGCT TGAGAAGCCC AGCCTGGAGC CTCAGAAGTC TCTGGGTGAC
1621 GAGGGCCTGA ACCGAGGCCC CTATGTTCTT GGACCTGCTG ACCGTGAGGA TGAGGAGGAA
1681 GATGAGGAAG AGGAGGAACA GACAGACCCC AAAAAGCCAA CTACAGATGA GGGCACAGCC
1741 AGCAGCGAGG TGAATGCCAC TGAGGAGATG TCCACGCTTG TCAACTACAT CGAACCTGTC
1801 AAGTTCAAGT CCTTTGAGGC TGCTCGAAAG AGGAACAAAT GCTTCGAGAT GTCGTCCTTT
1861 GTGGAGACCA AGGCCATGGA GCAACTGACC AAGAGCCCCA TGGAGTTTGT GGAATACAAC
1921 AAGCAGCAGC TCAGCCGCAT CTACCCCAAG GGCACCCGCG TGGACTCCTC CAACTACATG
1981 CCCCAGCTCT TCTGGAACGT AGGGTGCCAG CTTGTTGCGC TCAACTTCCA GACCCTCGAT
2041 GTGGCGATGC AGCTCAACGC GGGCGTTTTT GAGTACAACG GGCGCAGCGG GTACCTGCTC
2101 AAGCCGGAGT TCATGCGGCG GCCGGACAAG TCCTTCGACC CCTTCACTGA GGTCATCGTG
2161 GATGGCATCG TGGCCAATGC CTTGCGGGTC AAGGTGATCT CAGGGCAGTT CCTGTCCGAC
2221 AGGAAGGTGG GCATCTACGT GGAGGTGGAC ATGTTTGGCC TCCCTGTTGA TACGCGGCGC
2281 AAGTACCGCA CCCGGACCTC TCAGGGGAAC TCGTTCAACC CCGTGTGGGA CGAAGAGCCC
2341 TTCGACTTCC CCAAGGTGGT GCTGCCCACG CTGGCTTCAC TTCGCATTGC AGCCTTTGAG
2401 GAGGGGGGTA AATTCGTAGG GCACCGGATC CTGCCTGTCT CTGCCATCCG CTCCGGATAC
2461 CACTACGTCT GCCTGCGGAA CGAGGCCAAC CAACCGCTGT GCCTGCCGGC CCTGCTCATC
2521 TACACCGAAG CCTCGGACTA CATTCCTGAC GACCACCAGG ACTATGCGGA GGCCCTGATC
2581 AACCCCATTA AGCACGTCAG CCTGATGGAC CAGAGGGCCC GGCAGCTGGC CGCCCTCATT
2641 GGGGAGAGTG AGGCTCAGGC TGGCCAAGAG ACGTGCCAGG ACACCCAGTC TCAGCAGCTG
2701 GGGTCTCAGC CGTCCTCAAA CCCCACCCCC AGCCCACTGG ATGCCTCCCC CCGCCGGCCC
2761 CCTGGCCCCA CCACCTCCCC TGCCAGCACC TCCCTCAGCA GCCCAGGGCA GCGTGATGAT
2821 CTCATCGCCA GCATCCTCTC AGAGGTGGCC CCCACCCCGC TGGATGAGCT CCGAGGTCAC
2881 AAGGCTCTGG TCAAGCTCCG GAGCCGGCAA GAGCGAGACC TGCGGGAGCT GCGCAAGAAG
2941 CATCAGCGGA AGGCAGTCAC CCTCACCCGC CGCCTGCTGG ATGGCCTGGC TCAGGCACAG
3001 GCTGAGGGCA GGTGCCGGCT GCGGCCAGGT GCCCTAGGTG GGGCCGCTGA TGTGGAGGAC
3061 ACGAAGGAGG GGGAGGACGA GGCAAAGCGG TATCAGGAGT TCCAGAACAG ACAGGTGCAG
3121 AGCCTGCTGG AGCTGCGGGA GGCCCAGGTG GACGCAGAGG CCCAGCGGAG GCTGGAACAC
3181 CTGAGACAGG CTCTGCAGCG GCTCAGGGAG GTCGTCCTTG ATGCAAACAC AACTCAGTTC
3241 AAGAGGCTGA AAGAGATGAA CGAGAGGGAG AAGAAGGAGC TGCAGAAGAT CCTGGACAGA
3301 AAGCGCCATA ACAGCATCTC GGAGGCCAAG ATGAGGGACA AGCATAAGAA GGAGGCGGAA
3361 CTGACGGAGA TTAACCGTCG GCACATCACT GAGTCAGTCA ACTCCATCCG TCGGCTGGAG
3421 GAGGCCCAGA AGCAGCGGCA TGACCGTCTT GTGGCTGGGC AGCAGCAGGT CCTGCAACAG
3481 CTGGCAGAAG AGGAGCCCAA GCTGCTGGCC CAGCTGGCCC AGGAGTGTCA GGAGCAGCGG
3541 GCGAGGCTCC CCCAGGAGAT CCGCCGGAGC CTGCTGGGCG AGATGCCGGA GGGGCTGGGG
3601 GACGGGCCTC TGGTGGCCTG TGCCAGCAAC GGTCACGCAC CCGGGAGCAG CGGGCACCTG
3661 TCGGGCGCTG ACTCGGAGAG CCAGGAGGAG AACACGCAGC TCTGA
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GENBANK ID: D13119.1
DEFINITION  HOMO SAPIENS P2 MRNA FOR ATP SYNTHASE SUBUNIT C, COMPLETE CDS.
VERSION     D13119.1  GI:285909
CDS             31..456
/CODON_START=1

   1 TCTCCTGCCA CAGCTCCTCA CCCCCTGAAA ATGTTCGCCT GCTCCAAGTT TGTCTCCACT
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 121 AAACGACCGG AGATACTGAC AGATGAGAGC CTCAGCAGCT TGGCAGTCTC ATGTCCCCTT
 181 ACCTCACTTG TCTCTAGCCG CAGCTTCCAA ACCAGCGCCA TTTCAAGGGA CATCGACACA
 241 GCAGCCAAGT TCATTGGAGC TGGGGCTGCC ACAGTTGGGG TGGCTGGTTC TGGGGCTGGG
 301 ATTGGAACTG TGTTTGGGAG CCTCATCATT GGTTATGCCA GGAACCCTTC TCTGAAGCAA
 361 CAGCTCTTCT CCTACGCCAT TCTGGGCTTT GCCCTCTCGG AGGCCATGGG GCTCTTTTGT
 421 CTGATGGTAG CCTTTCTCAT CCTCTTTGCC ATGTGAAGGA GCCGTCTCCA CCTCCCATAG
 481 TTCTCCCGCG TCTGGTTGGC CCCGTGTGTT CCTTTTCCTA TACCTCCCCA GGCAGCCTGG
 541 GGAACGTGGT TGGCTCAGGG TTTGACAGAG AAAAGACAAA TAAATACTGT ATTAATAAG
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GENBANK ID:  NM_004530.1
DEFINITION  HOMO SAPIENS MATRIX METALLOPROTEINASE 2 (GELATINASE A, 72KD
            GELATINASE, 72KD TYPE IV COLLAGENASE) (MMP2), MRNA.
VERSION     NM_004530.1  GI:11342665
CDS             290..2272
/CODON_START=1
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   1 TGTTTCCGCT GCATCCAGAC TTCCTCAGGC GGTGGCTGGA GGCTGCGCAT CTGGGGCTTT
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 121 CGGGGGCCGG ACCATGAGCC GCTGAGCCGG GCAAACCCCA GGCCACCGAG CCAGCGGACC
 181 CTCGGAGCGC AGCCCTGCGC CGCGGACCAG GCTCCAACCA GGCGGCGAGG CGGCCACACG
 241 CACCGAGCCA GCGACCCCCG GGCGACGCGC GGGGCCAGGG AGCGCTACGA TGGAGGCGCT
 301 AATGGCCCGG GGCGCGCTCA CGGGTCCCCT GAGGGCGCTC TGTCTCCTGG GCTGCCTGCT
 361 GAGCCACGCC GCCGCCGCGC CGTCGCCCAT CATCAAGTTC CCCGGCGATG TCGCCCCCAA
 421 AACGGACAAA GAGTTGGCAG TGCAATACCT GAACACCTTC TATGGCTGCC CCAAGGAGAG
 481 CTGCAACCTG TTTGTGCTGA AGGACACACT AAAGAAGATG CAGAAGTTCT TTGGACTGCC
 541 CCAGACAGGT GATCTTGACC AGAATACCAT CGAGACCATG CGGAAGCCAC GCTGCGGCAA
 601 CCCAGATGTG GCCAACTACA ACTTCTTCCC TCGCAAGCCC AAGTGGGACA AGAACCAGAT
 661 CACATACAGG ATCATTGGCT ACACACCTGA TCTGGACCCA GAGACAGTGG ATGATGCCTT
 721 TGCTCGTGCC TTCCAAGTCT GGAGCGATGT GACCCCACTG CGGTTTTCTC GAATCCATGA
 781 TGGAGAGGCA GACATCATGA TCAACTTTGG CCGCTGGGAG CATGGCGATG GATACCCCTT
 841 TGACGGTAAG GACGGACTCC TGGCTCATGC CTTCGCCCCA GGCACTGGTG TTGGGGGAGA
 901 CTCCCATTTT GATGACGATG AGCTATGGAC CTTGGGAGAA GGCCAAGTGG TCCGTGTGAA
 961 GTATGGCAAC GCCGATGGGG AGTACTGCAA GTTCCCCTTC TTGTTCAATG GCAAGGAGTA
1021 CAACAGCTGC ACTGATACTG GCCGCAGCGA TGGCTTCCTC TGGTGCTCCA CCACCTACAA
1081 CTTTGAGAAG GATGGCAAGT ACGGCTTCTG TCCCCATGAA GCCCTGTTCA CCATGGGCGG
1141 CAACGCTGAA GGACAGCCCT GCAAGTTTCC ATTCCGCTTC CAGGGCACAT CCTATGACAG
1201 CTGCACCACT GAGGGCCGCA CGGATGGCTA CCGCTGGTGC GGCACCACTG AGGACTACGA
1261 CCGCGACAAG AAGTATGGCT TCTGCCCTGA GACCGCCATG TCCACTGTTG GTGGGAACTC
1321 AGAAGGTGCC CCCTGTGTCT TCCCCTTCAC TTTCCTGGGC AACAAATATG AGAGCTGCAC
1381 CAGCGCCGGC CGCAGTGACG GAAAGATGTG GTGTGCGACC ACAGCCAACT ACGATGACGA
1441 CCGCAAGTGG GGCTTCTGCC CTGACCAAGG GTACAGCCTG TTCCTCGTGG CAGCCCACGA
1501 GTTTGGCCAC GCCATGGGGC TGGAGCACTC CCAAGACCCT GGGGCCCTGA TGGCACCCAT
1561 TTACACCTAC ACCAAGAACT TCCGTCTGTC CCAGGATGAC ATCAAGGGCA TTCAGGAGCT
1621 CTATGGGGCC TCTCCTGACA TTGACCTTGG CACCGGCCCC ACCCCCACAC TGGGCCCTGT
1681 CACTCCTGAG ATCTGCAAAC AGGACATTGT ATTTGATGGC ATCGCTCAGA TCCGTGGTGA
1741 GATCTTCTTC TTCAAGGACC GGTTCATTTG GCGGACTGTG ACGCCACGTG ACAAGCCCAT
1801 GGGGCCCCTG CTGGTGGCCA CATTCTGGCC TGAGCTCCCG GAAAAGATTG ATGCGGTATA
1861 CGAGGCCCCA CAGGAGGAGA AGGCTGTGTT CTTTGCAGGG AATGAATACT GGATCTACTC
1921 AGCCAGCACC CTGGAGCGAG GGTACCCCAA GCCACTGACC AGCCTGGGAC TGCCCCCTGA
1981 TGTCCAGCGA GTGGATGCCG CCTTTAACTG GAGCAAAAAC AAGAAGACAT ACATCTTTGC
2041 TGGAGACAAA TTCTGGAGAT ACAATGAGGT GAAGAAGAAA ATGGATCCTG GCTTTCCCAA
2101 GCTCATCGCA GATGCCTGGA ATGCCATCCC CGATAACCTG GATGCCGTCG TGGACCTGCA
2161 GGGCGGCGGT CACAGCTACT TCTTCAAGGG TGCCTATTAC CTGAAGCTGG AGAACCAAAG
2221 TCTGAAGAGC GTGAAGTTTG GAAGCATCAA ATCCGACTGG CTAGGCTGCT GAGCTGGCCC
2281 TGGCTCCCAC AGGCCCTTCC TCTCCACTGC CTTCGATACA CCGGGCCTGG AGAACTAGAG
2341 AAGGACCCGG AGGGGCCTGG CAGCCGTGCC TTCAGCTCTA CAGCTAATCA GCATTCTCAC
2401 TCCTACCTGG TAATTTAAGA TTCCAGAGAG TGGCTCCTCC CGGTGCCCAA GAATAGATGC
2461 TGACTGTACT CCTCCCAGGC GCCCCTTCCC CCTCCAATCC CACCAACCCT CAGAGCCACC
2521 CCTAAAGAGA TCCTTTGATA TTTTCAACGC AGCCCTGCTT TGGGCTGCCC TGGTGCTGCC
2581 ACACTTCAGG CTCTTCTCCT TTCACAACCT TCTGTGGCTC ACAGAACCCT TGGAGCCAAT
2641 GGAGACTGTC TCAAGAGGGC ACTGGTGGCC CGACAGCCTG GCACAGGGCA GTGGGACAGG
2701 GCATGGCCAG GTGGCCACTC CAGACCCCTG GCTTTTCACT GCTGGCTGCC TTAGAACCTT
2761 TCTTACATTA GCAGTTTGCT TTGTATGCAC TTTGTTTTTT TCTTTGGGTC TTGTTTTTTT
2821 TTTCCACTTA GAAATTGCAT TTCCTGACAG AAGGACTCAG GTTGTCTGAA GTCACTGCAC
2881 AGTGCATCTC AGCCCACATA GTGATGGTTC CCCTGTTCAC TCTACTTAGC ATGTCCCTAC
2941 CGAGTCTCTT CTCCACTGGA TGGAGGAAAA CCAAGCCGTG GCTTCCCGCT CAGCCCTCCC
3001 TGCCCCTCCC TTCAACCATT CCCCATGGGA AATGTCAACA AGTATGAATA AAGACACCTA
3061 CTGAGTGGC
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GENBANK ID:  NM_000852.2
DEFINITION  HOMO SAPIENS GLUTATHIONE S-TRANSFERASE PI (GSTP1), MRNA.
VERSION     NM_000852.2  GI:6552334
CDS             30..662
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   1 GGAGTTTCGC CGCCGCAGTC TTCGCCACCA TGCCGCCCTA CACCGTGGTC TATTTCCCAG
  61 TTCGAGGCCG CTGCGCGGCC CTGCGCATGC TGCTGGCAGA TCAGGGCCAG AGCTGGAAGG
 121 AGGAGGTGGT GACCGTGGAG ACGTGGCAGG AGGGCTCACT CAAAGCCTCC TGCCTATACG
 181 GGCAGCTCCC CAAGTTCCAG GACGGAGACC TCACCCTGTA CCAGTCCAAT ACCATCCTGC
 241 GTCACCTGGG CCGCACCCTT GGGCTCTATG GGAAGGACCA GCAGGAGGCA GCCCTGGTGG
 301 ACATGGTGAA TGACGGCGTG GAGGACCTCC GCTGCAAATA CATCTCCCTC ATCTACACCA
 361 ACTATGAGGC GGGCAAGGAT GACTATGTGA AGGCACTGCC CGGGCAACTG AAGCCTTTTG
 421 AGACCCTGCT GTCCCAGAAC CAGGGAGGCA AGACCTTCAT TGTGGGAGAC CAGATCTCCT
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      481 TCGCTGACTA CAACCTGCTG GACTTGCTGC TGATCCATGA GGTCCTAGCC CCTGGCTGCC
      541 TGGATGCGTT CCCCCTGCTC TCAGCATATG TGGGGCGCCT CAGCGCCCGG CCCAAGCTCA
      601 AGGCCTTCCT GGCCTCCCCT GAGTACGTGA ACCTCCCCAT CAATGGCAAC GGGAAACAGT
      661 GAGGGTTGGG GGGACTCTGA GCGGGAGGCA GAGTTTGCCT TCCTTTCTCC AGGACCAATA
      721 AAATTTCTAA GAGAGCT
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GENBANK ID: XM_016524.4
DEFINITION HOMO SAPIENS CREATINE KINASE, MITOCHONDRIAL 1 (UBIQUITOUS) (CKMT1),MRNA.
VERSION XM_016524.4 GI:17477504
CDS 358..1704
/CODON_START=1

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        1 CGCGCGAGTC TCAGGTCCCG CTAATTACCT GGCGGGTGCT GCCCACCCCT GCCCTCGCGC
       61 ACCTAGCGCG GTGGCAGGCG GGAAGGCGGG GCCTGGGGGA GCCCCACCCC TGGAGACTGC
      121 GGCTGGGGCC TCCCTCTCCT CCGCCCGCCC GCCTGCCACT AGCTCATTGC GCCTCTCCTG
      181 CAGTCTGATT GGCACCGGCT CCCATTCCGG CTCCAGCCTC CAATCCGACC CCCATTTCGG
      241 CTGCAGCCTC GGACCTAGCT CCGGCCCTCG GTCTATCCGG TTGCATCCTC CCTCCCTGTT
      301 CCGGATCTTA TCTTGCGCCA GCGCCTACTC CAGGATCCCG TAGCCAGACC TCAAGCCATG
      361 GCTGGTCCCT TCTCCCGTCT GCTGTCCGCC CGCCCGGGAC TCAGGCTCCT GGCTTTGGCC
      421 GGAGCGGGGT CTCTAGCCGC TGGGTTTCTG CTCCGACCGG AACCTGTACG AGCTGCCAGT
      481 GAACGACGGA GGCTGTATCC CCCGAGCCAG ACATGGCCAA CTGGACAGCT CCCAGGTAAC
      541 TGCACTAGGT CTAGGCGTCT GTGCCCTCCC TCCATGGTTA CTGGGTACCC CCTCCCCAGC
      601 GCTGAGTACC CAGACCTCCG AAAGCACAAC AACTGCATGG CCAGTCACCT GACCCCAGCA
      661 GTCTATGCAC GGCTCTGCGA CAAGACCACA CCCACTGGTT GGACGCTAGA TCAGTGTATC
      721 CAGACTGGCG TGGACAACCC TGGCCACCCC TTCATCAAGA CTGTGGGCAT GGTGGCTGGA
      781 GATGAGGAGA CCTATGAGGT ATTTGCTGAC CTGTTTGACC CTGTGATCCA AGAGCGACAC
      841 AATGGATATG ACCCCCGGAC AATGAAGCAC ACCACGGATC TAGATGCCAG TAAAATCCGT
      901 TCTGGCTACT TTGATGAGAG GTATGTATTG TCCTCTAGAG TCAGAACTGG CCGAAGCATC
      961 CGAGGACTCA GTCTGCCTCC AGCTTGCACT CGAGCAGAGC GACGAGAGGT GGAACGTGTT
     1021 GTGGTGGATG CACTGAGTGG CCTGAAGGGT GACCTGGCTG GACGTTACTA TAGGCTCAGT
     1081 GAGATGACAG AGGCTGAACA GCAGCAGCTT ATTGATGACC ACTTTCTGTT TGATAAGCCT
     1141 GTGTCCCCGT TGCTGACTGC AGCAGGAATG GCTCGAGACT GGCCAGATGC TCGTGGAATT
     1201 TGGCACAACA ATGAGAAGAG CTTCCTGATC TGGGTGAATG AGGAGGATCA TACACGGGTG
     1261 ATCTCCATGG AGAAGGGTGG TAACATGAAG AGAGTGTTTG AAAGATTCTG CCGAGGCCTC
     1321 AAAGAGGTGG AGAGACTTAT CCAAGAACGT GGCTGGGAGT TCATGTGGAA TGAGCGTTTG
     1381 GGATACATCT TGACCTGTCC ATCTAACCTG GGCACTGGAC TTCGGGCAGG AGTGCACATC
     1441 AAACTGCCCC TGCTAAGCAA AGATAGCCGC TTCCCAAAGA TCCTGGAGAA CCTAAGACTC
     1501 CAAAAACGTG GTACTGGAGG AGTGGACACT GCTGCTACAG GCGGTGTCTT TGATATTTCT
     1561 AATTTGGACC GACTAGGCAA ATCAGAGGTG GAGCTGGTGC AACTGGTCAT CGATGGAGTA
     1621 AACTATTTGA TTGATTGTGA ACGGCGTCTG GAGAGAGGCC AGGATATCCG CATCCCCACA
     1681 CCTGTCATCC ACACCAAGCA TTAACTCCCC ATCGCCAGCT GATGACTCAA GATTCCCAGG
     1741 AGTTCTGCTC ATTCTAATGA TGGCCCATTC TACTTGCTCT GGACCTGCCC CCGCATCCCC
     1801 TGCCTCCATC CTAGTAAAGA CTCCTTGCTA TGCTGC
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GENBANK ID: NM_001443.1
DEFINITION HOMO SAPIENS FATTY ACID BINDING PROTEIN 1, LIVER (FABP1), MRNA.
VERSION NM_001443.1 GI:4557576
CDS 43..426

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        1 AGAGCCGCAG GTCAGTCGTG AAGAGGGAGC TCTATTGCCA CCATGAGTTT CTCCGGCAAG
       61 TACCAACTGC AGAGCCAGGA AAACTTTGAA GCCTTCATGA AGGCAATCGG TCTGCCGGAA
      121 GAGCTCATCC AGAAGGGGAA GGATATCAAG GGGGTGTCGG AAATCGTGCA GAATGGGAAG
      181 CACTTCAAGT TCACCATCAC CGCTGGGTCC AAAGTGATCC AAAACGAATT CACGGTGGGG
      241 GAGGAATGTG AGCTGGAGAC AATGACAGGG GAGAAAGTCA AGACAGTGGT TCAGTTGGAA
      301 GGTGACAATA AACTGGTGAC AACTTTCAAA AACATCAAGT CTGTGACCGA ACTCAACGGC
      361 GACATAATCA CCAATACCAT GACATTGGGT GACATTGTCT TCAAGAGAAT CAGCAAGAGA
      421 ATTTAAACAA GTCTGCATTT CATATTATTT TAGTGTGTAA AATTAATGTA ATAAAGTGAA
      481 CTTTGTTTT
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GENBANK ID: NM_001220.1
DEFINITION HOMO SAPIENS CALCIUM/CALMODULIN-DEPENDENT PROTEIN KINASE (CAM KINASE) II BETA (CAMK2B), MRNA.
VERSION NM_001220.1 GI:10835005
CDS 47..1675

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   1 GCGGCCCGCG TCGACCGAGC GCACGCCGAG CCCGTCCGCC GCCGCCATGG CCACCACGGT
  61 GACCTGCACC CGCTTCACCG ACGAGTACCA GCTCTACGAG GATATTGGCA AGGGGGCTTT
 121 CTCTGTGGTC CGACGCTGTG TCAAGCTCTG CACCGGCCAT GAGTATGCAG CCAAGATCAT
 181 CAACACCAAG AAGCTGTCAG CCAGAGATCA CCAGAAGCTG GAGAGAGAGG CTCGGATCTG
 241 CCGCCTTGTG AAGCATTCCA ACATCGTGCG TCTCCACGAC AGCATCTCCG AGGAGGGCTT
 301 CCACTACCTG GTCTTCGATC TGGTCACTGG TGGGGAGCTC TTTGAAGACA TTGTGGCGAG
 361 AGAGTACTAC AGCGAGGCTG ATGCCAGTCA CTGTATCCAG CAGATCCTGK AGGCCGTTCT
 421 CCATTGTCAC CAAATGGGGG TCGTCCACAG AGACCTCAAG CCGGAGAACC TGCTTCTGGC
 481 CAGCAAGTGC AAAGGGGCTG CAGTGAAGCT GGCAGACTTC GGCCTAGCTA TCGAGGTGCA
 541 GGGGGACCAG CAGGCATGGT TTGGTTTCGC TGGCACACCA GGCTACCTGT CCCCTGAGGT
 601 CCTTCGCAAA GAGGCGTACG GCAAGCCCGT GGACATCTGG GCATGTGGGG TGATCCTGTA
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1321 CAACAACGGT GACTTTGAGG CCTACGCGAA AATCTGTGAC CCAGGGCTGA CCTCGTTTGA
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GENBANK ID: NM_001677.1
DEFINITION HOMO SAPIENS ATPASE, NA+/K+ TRANSPORTING, BETA 1 POLYPEPTIDE (ATP1B1), MRNA.
VERSION NM_001677.1 GI:4502276
CDS 127..1038

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VERSION      U82535.1  GI:2149155
CDS              36..1775
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DEFINITION   HOMO SAPIENS DIPEPTIDYL CARBOXYPEPTIDASE 1 (ANGIOTENSIN I
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VERSION      NM_000789.1  GI:4503272
CDS              23..3943

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GENBANK ID: XM_052144.2
DEFINITION HOMO SAPIENS APOLIPOPROTEIN A-IV (APOA4), MRNA.
VERSION XM_052144.2 GI:15314431
CDS 114..1304
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GENBANK ID:  M29366.1
DEFINITION  HUMAN EPIDERMAL GROWTH FACTOR RECEPTOR (ERBB3) MRNA, COMPLETE CDS.
VERSION     M29366.1  GI:181979
CDS             100..4128
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4501 ACTGTCAAGA AGAGGAAAGG GAGGAAACCT AGCAGAGGAA AGTGTAATTT TGGTTTATGA
4561 CTCTTAACCC CCTAGAAAGA CAGAAGCTTA AAATCTGTGA AGAAAGAGGT TAGGAGTAGA
4621 TATTGATTAC TATCATAATT CAGCACTTAA CTATGAGCCA GGCATCATAC TAAACTTCAC
4681 CTACATTATC TCACTTAGTC CTTTATCATC CTTAAAACAA TTCTGTGACA TACATATTAT
4741 CTCATTTTAC ACAAAGGGAA GTCGGGCATG GTGGCTCATG CCTGTAATCT CAGCACTTTG
4801 GGAGGCTGAG GCAGAAGGAT TACCTGAGGC AAGGAGTTTG AGACCAGCTT AGCCAACATA
4861 GTAAGACCCC CATCTCTTT
```

GENBANK ID: X54686
VERSION X54686.1 GI:56909

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MCTKMEQAFYHDDSYAAAGYGRSPGSLSLHDYKLLKPTLALNLA
DPYRGLKGPGARGPGPEGSGAGSYFSGQGSDTGASLKLASTELERLIVPNSNGVITTT
PTPPGQYFYPRGGGSGGGTGGGVTEEQEGFADGFVKALDDLQKMNHVTPPNVSLGASG
GPQAGPGGVYAGPEPPPVYTNLSSYSPASAPSGGSGTAVGTGSSYPTATISYLPHAPP
FAGGHPAQLGLSRGASAFKEEPQTVPEARSRDATPPVSPINMEDQERIKVERKRLRNR
LAATKCRKRKLERIARLEDKVKTLKAENAGLSSAAGLLREQVAQLKQKVMTHVSNGCQ
LLLGVKGHAF
```

GENBANK ID: D26307
VERSION D26307.1 GI:450471

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METPFYGEEALSGLAAGASSVAGAAGAPGGGGFAPPGRAFPGAP
PTSSMLKKDALTLSLAEQGAAGLKPGSATAPSALRPDGAPDGLLASPDLGLLKLASPE
LERLIIQSNGLVTTTPTSTQFLYPKVAASEEQEFAEGFVKALEDLHKQSQLGAATAAT
SGAPAPPAPADLAATPGATETPVYANLSSFAGGAGPPGGAATVAFAAEPVPFPPPPGA
LGPPPPPHPPRLAALKDEPQTVPDVPSFGDSPPLSPIDMDTQERIKAERKRLRNRIAA
SKCRKRKLERISRLEEKVKTLKSQNTELASTASLLREQVAQLKQKVLSHVNSGCQLLP
QHQVPAY
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GENBANK ID: NM_012747.1
VERSION NM_012747.1 GI:6981591

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MAQWNQLQQLDTRYLEQLHQLYSDSFPMELRQFLAPWIESQDWA
YAASKESHATLVFHNLLGEIDQQYSRFLQESNVLYQHNLRRIKQFLQSRYLEKPMEIA
RIVARCLWEESRLLQTAATAAQQGGQANHPTAAVVTEKQQMLEQHLQDVRKRVQDLEQ
KMKVVENLQDDFDFNYKTLKSQGDMQDLNGNNQSVTRQKMQQLEQMLTALDQMRRSIV
SELAGLLSAMEYVQKTLTDEELADWKRRQQIACIGGPPNICLDRLENWITSLAESQLQ
TRQQIKKLEELQQKVSYKGDPIVQHRPMLEERIVDLFRNLMKSAFVVERQPCMPMHPD
RPLVIKTGVQFTTKVRLLVKFPELNYQLKIKVCIDKDSGDVAALRGSRKFNILGTNTK
VMNMEESNNGSLSAEFKHLTLREQRCGNGGRANCDASLIVTEELHLITFETEVYHQGL
KIDLETHSLPVVVISNICQMPNAWASILWYNMLTNNPKNVNFFTKPPIGTWDQVAEVL
SWQFSSTTKRGLSIEQLTTLAEKLLGPGVNYSGCQITWAKFCKENMAGKGFSFWVWLD
NIIDLVKKYILALWNEGYIMGFISKERERAILSTKPPGTFLLRFSESSKEGGVTFTWV
EKDISGKTQIQSVEPYTKQQLNNMSFAEIIMGYKIMDATNILVSPLVYLYPDIPKEEA
FGKYCRPESQEHPEADPGSAAPYLKTKFICVTPTTCSNTIDLPMSPRTLDSLMQFGNN
GEGAEPSAGGQFESLTFDMDLTSECATSPM
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GENBANK

ID: L26267.1
VERSION L26267.1 GI:425471

REILNPPEKETQGEGPSLFMASTKTEAIAPASTMEDKEEDVGFQ
DNLFLEKALQLAKRHANALFDYAVTGDVKMLLAVQRHLTAVQDENGDSVLHLAIIHLH
AQLVRDLLEVTSGSISDDIINMRNDLYQTPLHLAVITKQEDVVEDLLRVGADLSLLDR
WGNSVLHLAAKEGHDKILGVLLKNSKAALLINHPNGEGLNAIHIAVMSNSLSCLQLLV
AAGAEVNAQEQKSGRTALHLAVEYDNISLAGCLLLEGDALVDSTTYDGTTPLHIAAGR
GSTRLAALLKAAGADPLVENFEPLYDLDDSWEKAGEDEGVVPGTTPLDMAANWQVFDI
LNGKPYEPVFTSDDILPQGDIKQLTEDTRLQLCKLLEIPDPDKNWATLAQKLGLGILN
NAFRLSPAPSKTLMDNYEVSGGTIKELVEALRQMGYTEAIEVIQAAFRTPETTASSPV
TTAQAHLLPLSSSSTRQHIDELRDNDSVCDSGVETSFRKLSFSESLTGDGPLLSLNKM
PHNYGQDGPIEGKI

GENBANK ID:

M34356.1
VERSION M34356.1 GI:181042

MTMESGAENQQSGDAAVTEAENQQMTVQAQPQIATLAQVSMPAA
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SVTDSQKRREILSRRPSYRKILNDLSSDAPGVPRIEEEKSEEETSAPAITTVTVPTPI
YQTSSGQYIAITQGGAIQLANNGTDGVQGLQTLTMTNAAATQPGTTILQYAQTTDGQQ
ILVPSNQVVVQAASGDVQTYQIRTAPTSTIAPGVVMASSPALPTQPAEEAARKREVRL
MKNREAARECRRKKKEYVKCLENRVAVLENQNKTLIEELKALKDLYCHKSD

GENBANK ID:

X68193.1
VERSION X68193.1 GI:53353
MANLERTFIAIKPDGVQRGLVGEIIKRFEQKGFRLVAMKFLRAS
EEHLKQHYIDLKDRPFFPGLVKYMNSGPVVAMVWEGLNVVKTGRVMLGETNPADSKPG
TIRGDFCIQVGRNIIHGSDSVESAEKEIHLWFKPEELIDYKSCAHDWVYE

GENBANK

ID: U29200.1
VERSION U29200.1 GI:924934

MANLERTFIAIKPDGVQR

GENBANK ID: L35572
VERSION L35572.1 GI:531219

MMVHCAGCERPILDRFLLNVLDRAWHIKCVQCCECKTNLSEKCF
SREGKLYCKNDFFRRFGTKCAGCAQGISPSDLVRKARSKVFHLNCFTCMVCNKQLSTG
EELYVIDENKFVCKDDYLSSSSLKEGSLNSVSSCTDRSLSPDLQDPLQDDPKETDNST
SSDKETANNENEEQNSGTKRRGPRTTIKAKQLETLKAAFAATPKPTRHIREQLAQETG
LNMRVIQVWFQNRRSKERRMKQLSALGARRHAFFRSPRRMRPLGGRLDESEMLGSTPY
TYYGDYQSDYYAPGGNYDFFAHGPPSQAQSPADSSFLAASGPGSTPLGALEPPLAGPH
GADNPRFTDMISHPDTPSPEPGLPGALHPMPGEVFSGGPSPPFPMSGTSGYSGPLSHP
NPELNEAAVW

GENBANK ID: X55787.1
VERSION X55787.1 GI:296022
MKAAVDLKPTLTIIKTEKVDLELFPSPEMECADVPLSTPSSKEM
MSQALKSYFSGFTKEQQRRGIPKDPRQWTDTHVRDWVMWAVNEFSLKGVDFHKFCMSG
AAVCALGKECFLELAPDFVGDILWEHLEILQKEDVKPYQVNGANPTYPESCYTSVYFI
SYGIEHAQCVPPSEFSEPSFITESYQTLHPISSEELLSLKYENDYPSVILRDPLQTET
LQTDYFRIKQEVLTPNNMCLGRASRGKLGGQDSFESVESYDSCDRLTQSWSSQSSFNS
LQRVPSYDSFDYEDYPAALPNHKPKGTFKDYVRDRADLNKDKPVIPAAALAGYTGSGP
IQLWQFLLELLTDKSCQSFISWTGDCWEFKLSDPDEVARRWGKRKNKPSMNYEKLSRA
LRYYYDKNIIHKTAGNAYVYAFVCDLQSLLGYTPEELHAMLDVKPDAD

GENBANK ID: M11507.1
DEFINITION Human transferrin receptor

VERSION M11507.1 GI:339515

MMDQARSAFSNLFGGEPLSYTRFSLARQVDGDNSHVEMKLAVDE
EENADNNTKANVTKPKRCSGSICYGTIAVIVFFLIGFMIGYLGYCKGVEPKTECERLA
GTESPVREEPGEDFPAARRLYWDDLKRKLSEKLDSTDFTSTIKLLNENSYVPREAGSQ
KDENLALYVENQFREFKLSKVWRDQHFVKIQVKDSAQNSVIIVDKNGRLVYLVENPGG
YVAYSKAATVTGKLVHANFGTKKDFEDLYTPVNGSIVIVRAGKITFAEKVANAESLNA
IGVLIYMDQTKFPIVNAELSFFGHAHLGTGDPYTPGFPSFNHTQFPPSRSSGLPNIPV
QTISRAAAEKLFGNMEGDCPSDWKTDSTCRMVTSESKNVKLTVSNVLKEIKILNIFGV
IKGFVEPDHYVVVGAQRDAWGPGAAKSGVGTALLLKLAQMFSDMVLKDGFQPSRSIIF
ASWSAGDFGSVGATEWLEGYLSSLHLKAFTYINLDKAVLGTSNFKVSASPLLYTLIEK
TMQNVKHPVTGQFLYQDSNWASKVEKLTLDNAAFPFLAYSGIPAVSFCFCEDTDYPYL
GTTMDTYKELIERIPELNKVARAAAEVAGQFVIKLTHDVELNLDYERYNSQLLSFVRD
LNQYRADIKEMGLSLQWLYSARGDFFRATSRLTTDFGNAEKTDRFVMKKLNDRVMRVE
YHFLSPYVSPKESPFRHVFWGSGSHTLPALLENLKLRKQNNGAFNETLFRNQLALATW
TIQGAANALSGDVWDIDNEF

GENBANK ID: AAA60255
VERSION AAA60255.1 GI:190927

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   1 mteyklvvvg aggvgksalt iqliqnhfvd eydptiedsy rkqvvidget clldildtag
  61 qeeysamrdq ymrtgegflc vfainnsksf adinlyreqi krvkdsddvp mvlvgnkcdl
 121 ptrtvdtkqa helaksygip fietsaktrq gvedafytlv reirqyrmkk lnssddgtqg
 181 cmglpcvvm
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GENBANK ID: AAB38309
VERSION AAB38309.1 GI:1497931

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   1 mslvlndlli ccrqlehdra terkkevekf krlirdpeti khldrhsdsk qgkylnwdav
  61 frflqkyiqk eteclriakp nvsastqasr qkkmqeissl vkyfikcanr raprlkcqel
 121 lnyimdtvkd ssngaiygad csnillkdil svrkywceis qqqwlelfsv yfrlylkpsq
 181 dvhrvlvari ihavtkgccs qtdglnskfl dffskaiqca rqeksssgln hilaaltifl
 241 ktlavnfrir vcelgdeilp tllyiwtqhr lndslkevii elfqlqiyih hpkgaktqek
 301 gayestkwrs ilynlydllv neishigsrg kyssgfrnia vkenlielma dichqvfned
 361 trsleisqsy tttqressdy svpckrkkie lgwevikdhl qksqndfdlv pwlqiatqli
 421 skypaslpnc elspllmils qllpqqrhge rtpyvlrclt evalcqdkrs nlessqksdl
 481 lklwnkiwci tfrgisseqi qaenfgllga iiqgslvevd refwklftgs acrpscpavc
 541 cltlalttsi vpgtvkmgie qnmcevnrsf slkesimkwl lfyqlegdle nstevppilh
 601 snfphlvlek ilvsltmknc kaamnffqsv pecehhqkdk eelsfsevee lflqttfdkm
 661 dfltivrecg iekhqssigf svhqnlkesl drcllglseq llnnysseit nsetlvrcsr
 721 llvgvlgcyc ymgviaeeea ykselfqkak slmqcagesi tlfknktnee frigslrnmm
 781 qlctrclsnc tkkspnkias gfflrlltsk lmndiadick slasfikkpf drgevesmed
 841 dtngnlmeve dqssmnlfnd ypdssvsdan epgesqstig ainplaeeyl skqdllfldm
 901 lkflclcvtt aqtntvsfra adirrkllml idsstleptk slhlhmylml lkelpgeeyp
 961 lpmedvlell kplsnvcsly rrdqdvckti lnhvlhvvkn lgqsnmdsen trdaqgqflt
1021 vigafwhltk erkyifsvrm alvnclktll eadpyskwai lnvmgkdfpv nevftqflad
1081 nhhqvrmlaa esinrlfqdt kgdssrllka lplklqqtaf enaylkaqeg mremshsaen
1141 petldeiynr ksvlltliav vlscspicek qalfalcksv kenglephlv kkvlekvset
1201 fgyrrledfm ashldylvle wlnlqdteyn lssfpfilln ytniedfyrs cykvliphlv
1261 irshfdevks ianqiqedwk slltdcfpki lvnilpyfay egtrdsgmaq qretatkvyd
1321 mlksenllgk qidhlfisnl peivvellmt lhepanssas qstdlcdfsg dldpapnpph
1381 fpshvikatf ayisnchktk lksileilsk spdsyqkill aiceqaaetn nvykkhrilk
1441 iyhlfvslll kdiksglgga wafvlrdviy tlihyinqrp scimdvslrs fslccdllsq
1501 vcqtavtyck dalenhlhvi vgtliplvye qvevqkqvld llkylvidnk dnenlyitik
1561 lldpfpdhvv fkdlritqqk ikysrgpfsl leeinhflsv svydalpltr leglkdlrrq
1621 lelhkdqmvd imrasqdnpq dgimvklvvn llqlskmain htgekevlea vgsclgevgp
1681 idfstiaiqh skdasytkal klfedkelqw tfimltylnn tlvedcvkvr saavtclkni
1741 latktghsfw eiykmttdpm laylqpfrts rkkflevprf dkenpfegld dinlwiplse
1801 nhdiwiktlt cafldsggtk ceilqllkpm cevktdfcqt vlpylihdil lqdtneswrn
1861 llsthvqgff tsclrhfsqt srsttpanld sesehffrcc ldkksqrtml avvdymrrqk
1921 rpssgtifnd afwldlnyle vakvaqscaa hftallyaei yadkksmddq ekrslafeeg
1981 sqsttissls ekskeetgis lqdllleiyr sigepdslyg cgggkmlqpi trlrtyehea
2041 mwgkalvtyd letaipsstr qagiiqalqn lglchilsvy lkgldyenkd wcpeleelhy
2101 qaawrnmqwd hctsvskeve gtsyheslyn alqslrdref stfyeslkya rvkeveemck
2161 rslesvysly ptlsrlqaig elesigelfs rsvthrqlse vyikwqkhsq llkdsdfsfq
2221 epimalrtvi leilmekemd nsqrecikdi ltkhlvelsi lartfkntql peraifqikq
```

```
2281 ynsvscgvse wqleeaqvfw akkeqslals ilkqmikkld ascaannpsl kltyteclrv
2341 cgnwlaetcl enpavimqty lekavevagn ydgessdelr ngkmkaflsl arfsdtqyqr
2401 ienymkssef enkqallkra keevgllreh kiqtnrytvk vqreleldel alralkedrk
2461 rflckaveny incllsgeeh dmwvfrlcsl wlensgvsev ngmmkrdgmk iptykflplm
2521 yqlaarmgtk mmgglgfhev lnnlisrism dhphhtlfii lalananrde fltkpevarr
2581 sritknvpkq ssqldedrte aanriictir srrpqmvrsv ealcdayiil anldatqwkt
2641 qrkginipad qpitklknle dvvvptmeik vdhtgeygnl vtiqsfkaef rlaggvnlpk
2701 iidcvgsdgk errqlvkgrd dlrqdavmqq vfqmcntllq rntetrkrkl tictykvvpl
2761 sqrsgvlewc tgtvpigefl vnnedgahkr yrpndfsafq cqkkmmevqk ksfeekyevf
2821 mdvcqnfqpv fryfcmekfl dpaiwfekrl aytrsvatss ivgyilglgd rhvqniline
2881 qsaelvhidl gvafeqgkil ptpetvpfrl trdivdgmgi tgvegvfrrc cektmevmrn
2941 sqetlltive vllydplfdw tmnplkalyl qqrpedetel hptlnaddqe ckrnlsdidq
3001 sfdkvaervl mrlqeklkgv eegtvlsvgg qvnlliqqai dpknlsrlfp gwkawv
//

GENBANK ID: AAA59145.1
VERSION     AAA59145.1  GI:307058

   1 mlkpslpfts llflqlpllg vglnttiltp ngnedttadf flttmptdsl svstlplpev
  61 qcfvfnveym nctwnsssep qptnltlhyw yknsdndkvq kcshylfsee itsgcqlqkk
 121 eihlyqtfvv qlqdpreprr qatqmlklqn lvipwapenl tlhklsesql elnwnnrfln
 181 hclehlvqyr tdwdhswteq svdyrhkfsl psvdgqkryt frvrsrfnpl cgsaqhwsew
 241 shpihwgsnt skenpflfal eavvisvgsm gliisllcvy fwlertmpri ptlknledlv
 301 teyhgnfsaw sgvskglaes lqpdyserlc lvseippkgg algegpgasp cnqhspywap
 361 pcytlkpet

GENBANK ID: AAC50825.1
VERSION     AAC50825.1  GI:1117984

   1 mvaprplrrv vlfyqgklcs magnfwqssh ylqwildkqd llkerqkdlk flseeeywkl
  61 qifftnviqa lgehlklrqq viatatvyfk rfyarylslks idpvlmaptc vflaskveef
 121 gvvsntrlia aatsvlktrf syafpkefpy rmnhilecef yllelmdccl ivyhpyrpll
 181 qyvqdmgqed mllplawriv ndtyrtdlcl lyppfmiala clhvacvvqq kdarqwfael
 241 svdmekilei irvilklyeq wknfderkem atilskmpkp kpppnsegeq gpngsqnssy
 301 sqs

GENBANK ID: AAC50473.1
VERSION     AAC50473.1  GI:1314346

   1 mamssggsgg gvpeqedsvl frrgtgqsdd sdiwddtali kaydkavasf khalkngdic
  61 etsgkpkttp krkpakknks qkkntaaslq qwkvgdkcsa iwsedgciyp atiasidfkr
 121 etcvvvytgy gnreeqnlsd llspicevan nieqnaqene nesqvstdes ensrspgnks
 181 dnikpksapw nsflpppppm pgprlgpgkp glkfngpppp pppppphlls cwlppfpsgp
 241 piipppppic pdslddadal gsmliswyms gyhtgyymgf rqnqkegrcs hsln

GENBANK ID: CAC15525
VERSION     CAC15525.1  GI:11137517

   1 mvsrdqahlg pkyvglwdfk srtdeelsfr agdvfhvark eeqwwwatll deaggavaqg
  61 yvphnylaer etvesepwff gcisrseavr rlqaegnatg aflirvsekp sadyvlsvrd
 121 tqavrhykiw rraggrlhln eavsflslpe lvnyhraqsl shglrlaapc rkhepeplph
 181 wddwerpree ftlcrklgsg yfgevfeglw kdrvqvaikv isrdnllhqq mlqseiqamk
 241 klrhkhilal yavvsvgdpv yiitelmakg sllellrdsd ekvlpvsell diawqvaegm
 301 cylesqnyih rdlaarnilv gentlckvgd fglarliked vylshdhnip ykwtapeals
 361 rghystksdv wsfgillhem fsrgqvpypg msnheaflrv dagyrmpcpl ecppsvhklm
 421 ltcwcrdpeq rpcfkalrer lssftsyenp t
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GENBANK ID: AAB84296
VERSION AAB84296.1 GI:2613135

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  1 tsttvrglna strylfrvra svqglgdwsn tveettlglq saspvqesrv aedgldqqlv
 61 lavvgsvsat cltilaalla lvcirrsclh rrhtftyqsg sgeetilqfs sgtltltrrp
121 kpqpeplsyp vle
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GENBANK ID: X63594.1
VERSION X63594.1 GI:57673

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MFQPAGHGQDWAMEGPRDGLKKERLVDDRHDSGLDSMKDEDYEQ
MVKELREIRLQPQEAPLAAEPWKQQLTEDGDSFLHLAIIHEEKTLTMEVIGQVKGDLA
FLNFQNNLQQTPLHLAVITNQPGIAEALLKAGCDPELRDFRGNTPLHLACEQGCLASV
AVLTQTCTPQHLHSVLQATNYNGHTCLHLASIHGYLGIVEHLVTLGADVNAQEPCNGR
TALHLAVDLQNPDLVSLLLKCGADVNRVTYQGYSPYQLTWGRPSTRIQQQLGQLTLEN
LQTLPESEDEESYDTESEFTEDELPYDDCVFGGQRLTL
```

GENBANK ID: AAB60641

VERSION AAB60641.1 GI:516515

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  1 meqqdqsmke gmgttwllst pqhwlmqqfy netyygrtge fmedfpltll wsvtvsmfpf
 61 ggfigsllvg plvnkfgrkg allfnnifsi vpailmgcsr vatsfeliii srllvgicag
121 vssnvvpmyl gelapknlrg algvvpqlfi tvgilvaqif glrnllanvd gwpillgltg
181 vgaalqllll pffpespryl liqkkdeaaa kkalqtlrgw dsvdrevaei rqedeaekaa
241 gfisvlklfr mrslrwqlls iivlmggqql sgvnaiyyya dqiylsagvp eehvqyvtag
301 tgavnvvmtf cavfvvellg rrllllllgfs icliaccvlt aalalqdtvs wmpyisivcv
361 isyvighalg pspipallit eiflqssrps afmvggsvhw lsnftvglif pfiqeglgpy
421 sfivfavicl lttiyifliv petkaktfie inqiftkmnk vsevypekee lkelppvtse
481 q
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GENBANK ID: M29069
VERSION M29069.1 GI:205553

MLSCTTSTMPGMICKNSDLEFDSLKPCFYPEDDDIYFGGRNSTP
PGEDIWKKFELLPTPRLSPGRALAEDSLEPANWATEMLLPEADLWSNPAEEEDIFGLK
GLSGSSSNPVVLQDCMWSGFSSREKPETVVSEKLPGGCGSLAVGAGTLVPGAAAATSA
GHARSGTAGVGRRKAAWLTELSHLDSECVDSAVIFPANKRESMPVATIPASAGAAISL
GDHQGLSSSLEDFLSNSGYVEEGGEEIYVVMLGETQFSKTVTKLPTAAHSENAALTPE
CAQSGELILKRSDLIQEQHNYAAPPLPYAEDARPLKKPRSQDPLGPLKCVLRPKAPRL
RSRSNSDLEDIERRRNHNRMERQRRDIMRSSFLNLRDLVPELVHNEKAAKVVILKKAT
EYIHTLQTDESKLLVEREKLYERKQQLLEKIKQSAVC

GENBANK ID: M29039.1
VERSION M29039.1 GI:186626

MCTKMEQPFYHDDSYTATGYGRAPGGLSLHDYKLLKPSLAVNLA
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ATGGPPAGPGGVYAGPEPPPVYTNLSSYSPASASSGGAGAAVGTGSSYPTTTISYLPH
APPFAGGHPAQLGLGRGASTFKEEPQTVPEARSRDATPPVSPINMEDQERIKVERKRL
RNRLAATKCRKRKLERIARLEDKVKTLKAENAGLSSTAGLLREQVAQLKQKVMTHVSN
GCQLLLGVKGHAF

GENBANK ID: X56681.1
VERSION X56681.1 GI:34018

METPFYGDEALSGLGGGASGSGGTFASPGRLFPGAPPTAAAGSM
MKKDALTLSLSEQVAAALKPAPAPASYPPAADGAPSAAPPDGLLASPDLGLLKLASPE
LERLIIQSNGLVTTTPTSSQFLYPKVAASEEQEFAEGFVKALEDLHKQNQLGAGRAAA
AAAAAAGGPSGTATGSAPPGELAPAAAAPEAPVYANLSSYAGGAGGAGGAATVAFAAE
PVPFPPPPPPPGALGPPRLAALKDEPQTVPDVPSFGESPPLSPIDMDTQERIKAERKRL
RNRIAASKCRKRKLERISRLEEKVKTLKSQNTELASTASLLREQVAQLKQKVLSHVNS
GCQLLPQHQVPAY

GENBANK ID: NM_003150.1
VERSION NM_003150.1 GI:4507252

MAQWNQLQQLDTRYLEQLHQLYSDSFPMELRQFLAPWIESQDWA
YAASKESHATLVFHNLLGEIDQQYSRFLQESNVLYQHNLRRIKQFLQSRYLEKPMEIA
RIVARCLWEESRLLQTAATAAQQGGQANHPTAAVVTEKQQMLEQHLQDVRKRVQDLEQ
KMKVVENLQDDFDFNYKTLKSQGDMQDLNGNNQSVTRQKMQQLEQMLTALDQMRRSIV
SELAGLLSAMEYVQKTLTDEELADWKRRQQIACIGGPPNICLDRLENWITSLAESQLQ
TRQQIKKLEELHQKVSYKGDPIVQHRPMLEERIVELFRNLMKSAFVVERQPCMPMHPD
RPLVIKTGVQFTTKVRLLVKFPELNYQLKIKVCIDKDSGDVAALRGSRKFNILGTNTK
VMNMEESNNGSLSAEFKHLTLREQRCGNGGRANCDASLIVTEELHLITFETEVYHQGL
KIDLETHSLSVVVISNICQMPNAWASILWYNMLTNNPKNVNFFTKPPIGTWDQVAEVL
SWQFSSTTKRGLSIEQLTTLAEKLLGPGVNYSGCQITWANFCKENMAGKGFSYWVWLD
NIIDLVKKYILALWNEGYIMGFISKERERAILSTKPPGTFLLRFSESSKEGGVTFTWV
EKDISGKTQIQSVEPYTKQQLNNMSFAEIIMGYKIMDATNILLSPLVYLYPDIPKEEA
FGKYCRPESQEHPEADPGSAAPYLKTKFICVTPTTCSNTIDLPMSPRALDSLMQFGNN
GEGAEPSAGGQFESLTFDMELTSECATSPM

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Published:
— *with international search report*
— *before the expiration of the time limit for amending the claims and to be republished in the event of receipt of amendments*

(88) Date of publication of the international search report: 11 March 2004

For two-letter codes and other abbreviations, refer to the "Guidance Notes on Codes and Abbreviations" appearing at the beginning of each regular issue of the PCT Gazette.

(54) Title: GENETIC ANALYSIS OF PEYERS'S PATCHES AND M CELLS AND METHODS AND COMPOSITIONS TARGETING PEYER'S PATCHES AND M CELL RECEPTORS

(57) Abstract: Methods of increasing of or decreasing the levels of a protein in a PP cell; methods of increasing antigen, vaccine, DNA vaccine delivery to M cells, use of human serum albumin and other transport enhancing proteins to enhance oral drug delivery; use of calreticulin to enhance oral antigen delivery, use of other cell surface proteins, receptors, and transporters to enhance delivery to M cells of antigens or vaccine delivery vehicles, use of other cytoplasmic proteins to regulate intracellular trafficking and delivery to mucosal immune sampling and processing systems.

WO 2003/004646 A3

INTERNATIONAL SEARCH REPORT

International Application No
PCT/IB 02/03866

A. CLASSIFICATION OF SUBJECT MATTER
IPC 7 C12N15/12 C12N15/63 C07K14/00 A61K48/00 A61K47/42
A61K39/00 A61K47/48

According to International Patent Classification (IPC) or to both national classification and IPC

B. FIELDS SEARCHED

Minimum documentation searched (classification system followed by classification symbols)
IPC 7 A61K

Documentation searched other than minimum documentation to the extent that such documents are included in the fields searched

Electronic data base consulted during the international search (name of data base and, where practical, search terms used)
EPO-Internal, WPI Data, PAJ, MEDLINE, EMBASE, BIOSIS

C. DOCUMENTS CONSIDERED TO BE RELEVANT

Category *	Citation of document, with indication, where appropriate, of the relevant passages	Relevant to claim No.
X	US 6 060 082 A (CHEN HONGMING ET AL) 9 May 2000 (2000-05-09) column 1, line 11 - line 26 column 2, line 38 - line 47 column 2, line 66 - column 3, line 44 column 7, line 4 - line 33 column 19, line 31 - column 22, line 35 ----- -/--	1-58, 61-64

[X] Further documents are listed in the continuation of box C.

[X] Patent family members are listed in annex.

* Special categories of cited documents :

"A" document defining the general state of the art which is not considered to be of particular relevance

"E" earlier document but published on or after the international filing date

"L" document which may throw doubts on priority claim(s) or which is cited to establish the publication date of another citation or other special reason (as specified)

"O" document referring to an oral disclosure, use, exhibition or other means

"P" document published prior to the international filing date but later than the priority date claimed

"T" later document published after the international filing date or priority date and not in conflict with the application but cited to understand the principle or theory underlying the invention

"X" document of particular relevance; the claimed invention cannot be considered novel or cannot be considered to involve an inventive step when the document is taken alone

"Y" document of particular relevance; the claimed invention cannot be considered to involve an inventive step when the document is combined with one or more other such documents, such combination being obvious to a person skilled in the art.

"&" document member of the same patent family

Date of the actual completion of the international search	Date of mailing of the international search report
28 August 2003	07. 01. 2004

Name and mailing address of the ISA	Authorized officer
European Patent Office, P.B. 5818 Patentlaan 2 NL - 2280 HV Rijswijk Tel. (+31-70) 340-2040, Tx. 31 651 epo nl, Fax: (+31-70) 340-3016	Sitch, W

Form PCT/ISA/210 (second sheet) (July 1992)

INTERNATIONAL SEARCH REPORT

International Application No
PCT/IB 02/03866

C.(Continuation) DOCUMENTS CONSIDERED TO BE RELEVANT

Category °	Citation of document, with indication, where appropriate, of the relevant passages	Relevant to claim No.
X	GULLBERG ELISABET ET AL: "Expression of specific markers and particle transport in a new human intestinal M-cell model." BIOCHEMICAL AND BIOPHYSICAL RESEARCH COMMUNICATIONS, vol. 279, no. 3, 29 December 2000 (2000-12-29), pages 808-813, XP002252802 ISSN: 0006-291X page 808 abstract page 810, right-hand column, paragraph 1	59,60
A	US 6 117 632 A (O'MAHONY DANIEL JOSEPH) 12 September 2000 (2000-09-12) column 2, line 12 - line 40 column 3, line 48 - line 64	59,60
A	HADDAD A ET AL: "TARGETED M CELL IMMUNIZATION FOR HIV-1 ENV DNA VACCINES" FASEB JOURNAL, FED. OF AMERICAN SOC. FOR EXPERIMENTAL BIOLOGY, BETHESDA, MD, US, vol. 14, no. 6, 20 April 2000 (2000-04-20), page A1204, XP000995418 ISSN: 0892-6638 abstract 185.7	
E	WO 02/080852 A (O'MAHONY DANIEL J ;BRAYDEN DAVID J (IE); BYRNE DARAGH (IE); DIGITA) 17 October 2002 (2002-10-17) the whole document	1-58, 61-64

INTERNATIONAL SEARCH REPORT

International application No.
PCT/IB 02/03866

Box I Observations where certain claims were found unsearchable (Continuation of item 1 of first sheet)

This International Search Report has not been established in respect of certain claims under Article 17(2)(a) for the following reasons:

1. [X] Claims Nos.:
because they relate to subject matter not required to be searched by this Authority, namely:

Although partially claims 1-9, 12-21, 34-51, 61-64, and completely claims 10, 28-31, 33, are directed to a method of treatment of the human/animal body, the search has been carried out and based on the alleged effects of the compound/composition.

2. [X] Claims Nos.: 1-58, 61-64 partially
because they relate to parts of the International Application that do not comply with the prescribed requirements to such an extent that no meaningful International Search can be carried out, specifically:

see FURTHER INFORMATION sheet PCT/ISA/210

3. [ ] Claims Nos.:
because they are dependent claims and are not drafted in accordance with the second and third sentences of Rule 6.4(a).

Box II Observations where unity of invention is lacking (Continuation of item 2 of first sheet)

This International Searching Authority found multiple inventions in this international application, as follows:

see additional sheet

1. [ ] As all required additional search fees were timely paid by the applicant, this International Search Report covers all searchable claims.

2. [ ] As all searchable claims could be searched without effort justifying an additional fee, this Authority did not invite payment of any additional fee.

3. [ ] As only some of the required additional search fees were timely paid by the applicant, this International Search Report covers only those claims for which fees were paid, specifically claims Nos.:

4. [X] No required additional search fees were timely paid by the applicant. Consequently, this International Search Report is restricted to the invention first mentioned in the claims; it is covered by claims Nos.:

1-64

Remark on Protest

[ ] The additional search fees were accompanied by the applicant's protest.

[ ] No protest accompanied the payment of additional search fees.

FURTHER INFORMATION CONTINUED FROM PCT/ISA/ 210

Continuation of Box I.2

Claims Nos.: 1-58, 61-64 partially

Present claims 1-58 and 61-64 relate to an extremely large number of possible compounds and the use thereof. In the present particular case, there is considered to be support within the meaning of Article 6 PCT and/or disclosure within the meaning of Article 5 PCT for none of the compounds comprised in the claims. More particularly, there is a complete lack of evidence that the compounds recited in the claims provide any plausible solution to a technical problem possibly addressed by the application. Consequently, the claims are considered to so lack support, and the application to so lack disclosure, that a meaningful search over the whole of the claimed scope is impossible. As a result, the search has been carried out for those elements of the application which appear to be supported and disclosed, and for which a meaningful search was considered possible: in this particular case, a search was only considered possible on the inventive concept underlying the application, ie essentially that related to the correlation of altered expression of proteins in Peyer's patch cells / M cells with their use in enabling / facilitating oral delivery of drugs and antigens.

The applicant's attention is drawn to the fact that claims relating to inventions in respect of which no international search report has been established need not be the subject of an international preliminary examination (Rule 66.1(e) PCT). The applicant is advised that the EPO policy when acting as an International Preliminary Examining Authority is normally not to carry out a preliminary examination on matter which has not been searched. This is the case irrespective of whether or not the claims are amended following receipt of the search report or during any Chapter II procedure. If the application proceeds into the regional phase before the EPO, the applicant is reminded that a search may be carried out during examination before the EPO (see EPO Guideline C-VI, 8.5), should the problems which led to the Article 17(2) declaration be overcome.

FURTHER INFORMATION CONTINUED FROM PCT/ISA/ 210

This International Searching Authority found multiple (groups of) inventions in this international application, as follows:

1. claims: 1-64

Means to increase in PP cells of the intestine levels of proteins specific to PP cells, or decrease in PP cells of the intestine the levels of proteins non-specific to PP cells, via delivery of a nucleic acid encoding the PP cell specific protein / the protein per se, or delivery of an antisense / ribozyme / RNAi to the protein non-specific to PP cells, (eg claim 1 et seq., claim 15 and seq.); means to deliver a composition to a PP cell wherein said composition has a ligand that will specifically bind to a PP specific protein (eg claim 57); related subject matter

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2. claim: 65

Promote enterocyte-M cell conversion via use of an antigen and a bacteria, probiotic yoghurt or bacterial component

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INTERNATIONAL SEARCH REPORT

Information on patent family members

International Application No
PCT/IB 02/03866

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